



PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/00	A2	(11) International Publication Number: WO 99/58658 (43) International Publication Date: 18 November 1999 (18.11.99)
(21) International Application Number: PCT/US99/10646		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
(22) International Filing Date: 13 May 1999 (13.05.99)		
(30) Priority Data: 09/078,904 13 May 1998 (13.05.98) US 60/085,751 15 May 1998 (15.05.98) US		
(71) Applicant: EPIMMUNE, INC. [US/US]; Suite 100, 5820 Nancy Ridge Drive, San Diego, CA 92121 (US).		
(72) Inventors: FIKES, John, D.; 6474 Lippmann Street, San Diego, CA 92122 (US). HERMANSON, Gary, G.; 3159 Via de Caballo, Encinitas, CA 92024 (US). SETTE, Alessandro; 5551 Linda Rosa Avenue, La Jolla, CA 92037 (US). ISHIOKA, Glenn, Y.; Apartment J5, 725 South Nardo Avenue, Solana Beach, CA 92075 (US). LIVINGSTON, Brian; 13555 Chaco Court, San Diego, CA 92129 (US). CHESNUT, Robert, W.; 1473 Kings Cross Drive, Cardiff-by-the-Sea, CA 92007 (US).		Published <i>Without international search report and to be republished upon receipt of that report.</i>
(74) Agents: PARENT, Annette, S. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).		
(54) Title: EXPRESSION VECTORS FOR STIMULATING AN IMMUNE RESPONSE AND METHODS OF USING THE SAME		
(57) Abstract		
The present invention relates to nucleic acid vaccines encoding multiple CTL and HTL epitopes and MHC targeting sequences.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

EXPRESSION VECTORS FOR STIMULATING AN IMMUNE RESPONSE AND METHODS OF USING THE SAME

CROSS-REFERENCES TO RELATED APPLICATIONS

5 This application claims the benefit of 09/078,904, filed May 13, 1998, and 60/085,751, filed May 15, 1998, both herein incorporated by reference in their entirety.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

10 This invention was made with government support under NIH Grant No. AI-42699-01, NIH Grant No. AI38584-03, and NIH Contract No. N01-AI-45241. The Government has certain rights in this invention.

FIELD OF THE INVENTION

15 The present invention relates to nucleic acid vaccines encoding multiple CTL and HTL epitopes and MHC targeting sequences.

BACKGROUND OF THE INVENTION

Vaccines are of fundamental importance in modern medicine and have
20 been highly effective in combating certain human diseases. However, despite the successful implementation of vaccination programs that have greatly limited or virtually eliminated several debilitating human diseases, there are a number of diseases that affect millions worldwide for which effective vaccines have not been developed.

Major advances in the field of immunology have led to a greater
25 understanding of the mechanisms involved in the immune response and have provided insights into developing new vaccine strategies (Kuby, *Immunology*, 443-457 (3rd ed., 1997), which is incorporated herein by reference). These new vaccine strategies have taken advantage of knowledge gained regarding the mechanisms by which foreign material, termed antigen, is recognized by the immune system and eliminated from the
30 organism. An effective vaccine is one that elicits an immune response to an antigen of interest.

Specialized cells of the immune system are responsible for the protective activity required to combat diseases. An immune response involves two major groups of cells, lymphocytes, or white blood cells, and antigen-presenting cells. The purpose of

these immune response cells is to recognize foreign material, such as an infectious organism or a cancer cell, and remove that foreign material from the organism.

Two major types of lymphocytes mediate different aspects of the immune response. B cells display on their cell surface specialized proteins, called antibodies, that bind specifically to foreign material, called antigens. Effector B cells produce soluble forms of the antibody, which circulate throughout the body and function to eliminate antigen from the organism. This branch of the immune system is known as the humoral branch. Memory B cells function to recognize the antigen in future encounters by continuing to express the membrane-bound form of the antibody.

A second major type of lymphocyte is the T cell. T cells also have on their cell surface specialized proteins that recognize antigen but, in contrast to B cells, require that the antigen be bound to a specialized membrane protein complex, the major histocompatibility complex (MHC), on the surface of an antigen-presenting cell. Two major classes of T cells, termed helper T lymphocytes ("HTL") and cytotoxic T lymphocytes ("CTL"), are often distinguished based on the presence of either CD4 or CD8 protein, respectively, on the cell surface. This branch of the immune system is known as the cell-mediated branch.

The second major class of immune response cells are cells that function in antigen presentation by processing antigen for binding to MHC molecules expressed in the antigen presenting cells. The processed antigen bound to MHC molecules is transferred to the surface of the cell, where the antigen-MHC complex is available to bind to T cells.

MHC molecules can be divided into MHC class I and class II molecules and are recognized by the two classes of T cells. Nearly all cells express MHC class I molecules, which function to present antigen to cytotoxic T lymphocytes. Cytotoxic T lymphocytes typically recognize antigen bound to MHC class I. A subset of cells called antigen-presenting cells express MHC class II molecules. Helper T lymphocytes typically recognize antigen bound to MHC class II molecules. Antigen-presenting cells include dendritic cells, macrophages, B cells, fibroblasts, glial cells, pancreatic beta cells, thymic epithelial cells, thyroid epithelial cells and vascular endothelial cells. These antigen-presenting cells generally express both MHC class I and class II molecules. Also, B cells function as both antibody-producing and antigen-presenting cells.

Once a helper T lymphocyte recognizes an antigen-MHC class II complex on the surface of an antigen-presenting cell, the helper T lymphocyte becomes activated

and produces growth factors that activate a variety of cells involved in the immune response, including B cells and cytotoxic T lymphocytes. For example, under the influence of growth factors expressed by activated helper T lymphocytes, a cytotoxic T lymphocyte that recognizes an antigen-MHC class I complex becomes activated. CTLs 5 monitor and eliminate cells that display antigen specifically recognized by the CTL, such as infected cells or tumor cells. Thus, activation of helper T lymphocytes stimulates the activation of both the humoral and cell-mediated branches of the immune system.

An important aspect of the immune response, in particular as it relates to vaccine efficacy, is the manner in which antigen is processed so that it can be recognized 10 by the specialized cells of the immune system. Distinct antigen processing and presentation pathways are utilized. The one is a cytosolic pathway, which results in the antigen being bound to MHC class I molecules. An alternative pathway is an endoplasmic reticulum pahtway, which bypasses the cytosol. Another is an endocytic pathway, which results in the antigen being bound to MHC class II molecules. Thus, the 15 cell surface presentation of a particular antigen by a MHC class II or class I molecule to a helper T lymphocyte or a cytotoxic T lymphocyte, respectively, is dependent on the processing pathway for that antigen.

The cytosolic pathway processes endogenous antigens that are expressed 20 inside the cell. The antigen is degraded by a specialized protease complex in the cytosol of the cell, and the resulting antigen peptides are transported into the endoplasmic reticulum, an organelle that processes cell surface molecules. In the endoplasmic reticulum, the antigen peptides bind to MHC class I molecules, which are then transported to the cell surface for presentation to cytotoxic T lymphocytes of the immune system.

25 Antigens that exist outside the cell are processed by the endocytic pathway. Such antigens are taken into the cell by endocytosis, which brings the antigens into specialized vesicles called endosomes and subsequently to specialized vesicles called lysosomes, where the antigen is degraded by proteases into antigen peptides that bind to MHC class II molecules. The antigen peptide-MHC class II molecule complex is then 30 transported to the cell surface for presentation to helper T lymphocytes of the immune system.

A variety of factors must be considered in the development of an effective vaccine. For example, the extent of activation of either the humoral or cell-mediated branch of the immune system can determine the effectiveness of a vaccine against a

particular disease. Furthermore, the development of immunologic memory by inducing memory-cell formation can be important for an effective vaccine against a particular disease (*Kuby, supra*). For example, protection from infectious diseases caused by pathogens with short incubation periods, such as influenza virus, requires high levels of 5 neutralizing antibody generated by the humoral branch because disease symptoms are already underway before memory cells are activated. Alternatively, protection from infectious diseases caused by pathogens with long incubation periods, such as polio virus, does not require neutralizing antibodies at the time of infection but instead requires memory B cells that can generate neutralizing antibodies to combat the pathogen before it 10 is able to infect target tissues. Therefore, the effectiveness of a vaccine at preventing or ameliorating the symptoms of a particular disease depends on the type of immune response generated by the vaccine.

Many traditional vaccines have relied on intact pathogens such as attenuated or inactivated viruses or bacteria to elicit an immune response. However, 15 these traditional vaccines have advantages and disadvantages, including reversion of an attenuated pathogen to a virulent form. The problem of reversion of an attenuated vaccine has been addressed by the use of molecules of the pathogen rather than the whole pathogen. For example, immunization approaches have begun to incorporate recombinant vector vaccines and synthetic peptide vaccines (*Kuby, supra*). Recently, 20 DNA vaccines have also been used (Donnelly *et al.*, *Annu. Rev. Immunol.* 15:617-648 (1997), which is incorporated herein by reference). The use of molecules of a pathogen provides safe vaccines that circumvent the potential for reversion to a virulent form of the vaccine.

The targeting of antigens to MHC class II molecules to activate helper T 25 lymphocytes has been described using lysosomal targeting sequences, which direct antigens to lysosomes, where the antigen is digested by lysosomal proteases into antigen peptides that bind to MHC class II molecules (U.S. Patent No. 5,633,234; Thomson *et al.*, *J. Virol.* 72:2246-2252 (1998)). It would be advantageous to develop vaccines that deliver multiple antigens while exploiting the safety provided by administering individual 30 epitopes of a pathogen rather than a whole organism. In particular, it would be advantageous to develop vaccines that effectively target antigens to MHC class II molecules for activation of helper T lymphocytes.

Several studies also point to the crucial role of cytotoxic T cells in both production and eradication of infectious diseases and cancer by the immune system

(Byrne *et al.*, *J. Immunol.* 51:682 (1984); McMichael *et al.*, *N. Engl. J. Med.* 309:13 (1983)). Recombinant protein vaccines do not reliably induce CTL responses, and the use of otherwise immunogenic vaccines consisting of attenuated pathogens in humans is hampered, in the case of several important diseases, by overriding safety concerns. In the 5 case of diseases such as HIV, HBV, HCV, and malaria, it appears desirable not only to induce a vigorous CTL response, but also to focus the response against highly conserved epitopes in order to prevent escape by mutation and overcome variable vaccine efficacy against different isolates of the target pathogen.

Induction of a broad response directed simultaneously against multiple 10 epitopes also appears to be crucial for development of efficacious vaccines. HIV infection is perhaps the best example where an infected host may benefit from a multispecific response. Rapid progression of HIV infection has been reported in cases where a narrowly focused CTL response is induced whereas nonprogressors tend to show a broader specificity of CTLs (Goulder *et al.*, *Nat. Med.* 3:212 (1997); Borrow *et al.*, *Nat. Med.* 3:205 (1997)). The highly variable nature of HIV CTL epitopes resulting from a 15 highly mutating genome and selection by CTL responses directed against only a single or few epitopes also supports the need for broad epitope CTL responses (McMichael *et al.*, *Annu. Rev. Immunol.* 15:271 (1997)).

One potential approach to induce multispecific responses against 20 conserved epitopes is immunization with a minigene plasmid encoding the epitopes in a string-of-beads fashion. Induction of CTL, HTL, and B cell responses in mice by minigene plasmids have been described by several laboratories using constructs encoding as many as 11 epitopes (An *et al.*, *J. Virol.* 71:2292 (1997); Thomson *et al.*, *J. Immunol.* 157:822 (1996); Whitton *et al.*, *J. Virol.* 67:348 (1993); Hanke *et al.*, *Vaccine* 16:426 25 (1998); Vitiello *et al.*, *Eur. J. Immunol.* 27:671-678 (1997)). Minigenes have been delivered *in vivo* by infection with recombinant adenovirus or vaccinia, or by injection of purified DNA via the intramuscular or intradermal route (Thomson *et al.*, *J. Immunol.* 160:1717 (1998); Toes *et al.*, *Proc. Natl. Acad. Sci. USA* 94:14660 (1997)).

Successful development of minigene DNA vaccines for human use will 30 require addressing certain fundamental questions dealing with epitope MHC affinity, optimization of constructs for maximum *in vivo* immunogenicity, and development of assays for testing *in vivo* potency of multi-epitope minigene constructs. Regarding MHC binding affinity of epitopes, it is not currently known whether both high and low affinity epitopes can be included within a single minigene construct, and what ranges of peptide

affinity are permissible for CTL induction *in vivo*. This is especially important because dominant epitopes can vary in their affinity and because it might be important to be able to deliver mixtures of dominant and subdominant epitopes that are characterized by high and low MHC binding affinities.

5 With respect to minigene construct optimization for maximum immunogenicity *in vivo*, conflicting data exists regarding whether the exact position of the epitopes in a given construct or the presence of flanking regions, helper T cell epitopes, and signal sequences might be crucial for CTL induction (Del Val *et al.*, *Cell* 66:1145 (1991); Bergmann *et al.*, *J. Virol.* 68:5306 (1994); Thomson *et al.*, *Proc. Natl. Acad. Sci. USA* 92:5845 (1995); Shirai *et al.*, *J. Infect. Dis.* 173:24 (1996); Rahemtulla *et al.*, *Nature* 353:180 (1991); Jennings *et al.*, *Cell. Immunol.* 133:234 (1991); Anderson *et al.*, *J. Exp. Med.* 174:489 (1991); Uger *et al.*, *J. Immunol.* 158:685 (1997)). Finally, regarding development of assays that allow testing of human vaccine candidates, it should be noted that, to date, all *in vivo* immunogenicity data of multi-epitope minigene plasmids 10 have been performed with murine class I MHC-restricted epitopes. It would be 15 advantageous to be able to test the *in vivo* immunogenicity of minigenes containing human CTL epitopes in a convenient animal model system.

Thus, there exists a need to develop methods to effectively deliver a variety of HTL (helper T lymphocyte) and CTL (cytotoxic T lymphocyte) antigens to 20 stimulate an immune response. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF THE INVENTION

The invention therefore provides expression vectors encoding two or more 25 HTL epitopes fused to a MHC class II targeting sequence, as well as expression vectors encoding a CTL epitope and a universal HTL epitope fused to an MHC class I targeting sequence. The HTL epitope can be a universal HTL epitope (also referred to as a universal MHC class II epitope). The invention also provides expression vectors 30 encoding two or more HTL epitopes fused to a MHC class II targeting sequence and encoding one or more CTL epitopes. The invention additionally provides methods of stimulating an immune response by administering an expression vector of the invention *in vivo*, as well as methods of assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in a non-human mammal.

In one aspect, the present invention provides an expression vector comprising a promoter operably linked to a first nucleotide sequence encoding a major histocompatibility (MHC) targeting sequence fused to a second nucleotide sequence encoding two or more heterologous peptide epitopes, wherein the heterologous peptide epitopes comprise two HTL peptide epitopes or a CTL peptide epitope and a universal HTL peptide epitope.

5 In another aspect, the present invention provides a method of inducing an immune response *in vivo* comprising administering to a mammalian subject an expression vector comprising a promoter operably linked to a first nucleotide sequence encoding a major histocompatibility (MHC) targeting sequence fused to a second nucleotide sequence encoding two or more heterologous peptide epitopes, wherein the heterologous peptide epitopes comprise two HTL peptide epitopes or a CTL peptide epitope and a universal HTL peptide epitope.

10 15 In another aspect, the present invention provides a method of inducing an immune response *in vivo* comprising administering to a mammalian subject an expression vector comprising a promoter operably linked to a first nucleotide sequence encoding a major histocompatibility (MHC) targeting sequence fused to a second nucleotide sequence encoding a heterologous human HTL peptide epitope.

20 In another aspect, the present invention provides a method of assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in a non-human mammal, comprising the step of administering to the non-human mammal an expression vector comprising a promoter operably linked to a first nucleotide sequence encoding a heterologous human CTL or HTL peptide epitope.

25 In one embodiment, the heterologous peptide epitopes comprise two or more heterologous HTL peptide epitopes. In another embodiment, the heterologous peptide epitopes comprise a CTL peptide epitope and a universal HTL peptide epitope. In another embodiment, the heterologous peptide epitopes further comprise one to two or more heterologous CTL peptide epitopes. In another embodiment, the expression vector comprises both HTL and CTL peptide epitopes.

30 In one embodiment, one of the HTL peptide epitopes is a universal HTL epitope. In another embodiment, the universal HTL epitope is a pan DR epitope. In another embodiment, the pan DR epitope has the sequence AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38).

In one embodiment, the peptide epitopes are hepatitis B virus epitopes, hepatitis C virus epitopes, human immunodeficiency virus epitopes, human papilloma virus epitopes, MAGE epitopes, PSA epitopes, PSM epitopes, PAP epitopes, p53 epitopes, CEA epitopes, Her2/neu epitopes, or *Plasmodium* epitopes. In another embodiment, the peptide epitopes each have a sequence selected from the group consisting of the peptides depicted in Tables 1-8. In another embodiment, at least one of the peptide epitopes is an analog of a peptide depicted in Tables 1-8.

5 In one embodiment, the MHC targeting sequence comprises a region of a polypeptide selected from the group consisting of the Ii protein, LAMP-I, HLS-DM, HLA-DO, H2-DO, influenza matrix protein, hepatitis B surface antigen, hepatitis B virus core antigen, Ty particle, Ig- α protein, Ig- β protein, and Ig kappa chain signal sequence.

10 In one embodiment, the expression vector further comprises a second promoter sequence operably linked to a third nucleotide sequence encoding one or more heterologous HTL or CTL peptide epitopes. In another embodiment, the CTL peptide epitope comprises a structural motif for an HLA supertype, whereby the peptide CTL 15 epitope binds to two or more members of the supertype with an affinity of greater than 500 nM. In another embodiment, the CTL peptide epitopes have structural motifs that provide binding affinity for more than one HLA allele supertype.

15 In one embodiment, the non-human mammal is a transgenic mouse that expresses a human HLA allele. In another embodiment, the human HLA allele is selected 20 from the group consisting of A11 and A2.1. In another embodiment, the non-human mammal is a macaque that expresses a human HLA allele.

BRIEF DESCRIPTION OF THE DRAWINGS

25 Figure 1 shows the nucleotide and amino acid sequences (SEQ ID NOS:1 and 2, respectively) of the LiPADRE construct encoding a fusion of the murine Ii gene with a pan DR epitope sequence substituted for the CLIP sequence of the Ii protein.

Figure 2 shows the nucleotide and amino acid sequences (SEQ ID NOS:3 and 4, respectively) of the I80T construct encoding a fusion of the cytoplasmic domain, 30 the transmembrane domain and part of the luminal domain of the Ii protein fused to multiple MHC class II epitopes.

Figure 3 shows the nucleotide and amino acid sequences (SEQ ID NOS:5 and 6, respectively) of the IiThfull construct encoding a fusion of the cytoplasmic domain, transmembrane domain and a portion of the luminal domain of the Ii protein

fused to multiple T helper epitopes and amino acid residues 101 to 215 of the Ii protein, which encodes the trimerization region of the Ii protein.

Figure 4 shows the nucleotide and amino acid sequences (SEQ ID NOS:7 and 8, respectively) of the KappaLAMP-Th construct encoding a fusion of the murine immunoglobulin kappa signal sequence fused to multiple T helper epitopes and the transmembrane and cytoplasmic domains of LAMP-1.

Figure 5 shows the nucleotide and amino acid sequences (SEQ ID NOS:9 and 10, respectively) of the H2M-Th construct encoding a fusion of the signal sequence of H2-M fused to multiple MHC class II epitopes and the transmembrane and cytoplasmic domains of H2-M.

Figure 6 shows the nucleotide and amino acid sequences (SEQ ID NOS:11 and 12, respectively) of the H2O-Th construct encoding a fusion of the signal sequence of H2-DO fused to multiple MHC class II epitopes and the transmembrane and cytoplasmic domains of H2-DO.

Figure 7 shows the nucleotide and amino acid sequences (SEQ ID NOS:13 and 14, respectively) of the PADRE-Influenza matrix construct encoding a fusion of a pan DR epitope sequence fused to the amino-terminus of influenza matrix protein.

Figure 8 shows the nucleotide and amino acid sequences (SEQ ID NOS:15 and 16, respectively) of the PADRE-HBV-s construct encoding a fusion of a pan DR epitope sequence fused to the amino-terminus of hepatitis B virus surface antigen.

Figure 9 shows the nucleotide and amino acid sequences (SEQ ID NOS:17 and 18, respectively) of the Ig-alphaTh construct encoding a fusion of the signal sequence of the Ig- α protein fused to multiple MHC class II epitopes and the transmembrane and cytoplasmic domains of the Ig- α protein.

Figure 10 shows the nucleotide and amino acid sequences (SEQ ID NOS:19 and 20, respectively) of the Ig-betaTh construct encoding a fusion of the signal sequence of the Ig- β protein fused to multiple MHC class II epitopes and the transmembrane and cytoplasmic domains of the Ig- β protein.

Figure 11 shows the nucleotide and amino acid sequences (SEQ ID NOS:21 and 22, respectively) of the SigTh construct encoding a fusion of the signal sequence of the kappa immunoglobulin fused to multiple MHC class II epitopes.

Figure 12 shows the nucleotide and amino acid sequences (SEQ ID NOS:23 and 24, respectively) of human HLA-DR, the invariant chain (Ii) protein.

Figure 13 shows the nucleotide and amino acid sequences (SEQ ID NOS:25 and 26, respectively) of human lysosomal membrane glycoprotein-1 (LAMP-1).

Figure 14 shows the nucleotide and amino acid sequences (SEQ ID NOS:27 and 28, respectively) of human HLA-DMB.

5 Figure 15 shows the nucleotide and amino acid sequences (SEQ ID NOS:29 and 30, respectively) of human HLA-DO beta.

Figure 16 shows the nucleotide and amino acid sequences (SEQ ID NOS:31 and 32, respectively) of the human MB-1 Ig-a.

10 Figure 17 shows the nucleotide and amino acid sequences (SEQ ID NOS:33 and 34, respectively) of human Ig- β protein.

Figure 18 shows a schematic diagram depicting the method of generating some of the constructs encoding a MHC class II targeting sequence fused to multiple MHC class II epitopes.

15 Figure 19 shows the nucleotide sequence of the vector pEP2 (SEQ ID NO:35).

Figure 20 shows the nucleotide sequence of the vector pMIN.0 (SEQ ID NO:36).

Figure 21 shows the nucleotide sequence of the vector pMIN.1 (SEQ ID NO:37).

20 Figure 22. Representative CTL responses in HLA-A2.1/K^b-H-2^{bxs} mice immunized with pMin.1 DNA. Splenocytes from primed animals were cultured in triplicate flasks and stimulated twice *in vitro* with each peptide epitope. Cytotoxicity of each culture was assayed in a ⁵¹Cr release assay against Jurkat-A2.1/K^b target cells in the presence (filled symbols, solid lines) or absence (open symbols, dotted lines) of peptide.

25 Each symbol represents the response of a single culture.

Figure 23. Presentation of viral epitopes to specific CTLs by Jurkat-A2.1/K^b tumor cells transfected with DNA minigene. Two constructs were used for transfection, pMin.1 and pMin.2-GFP. pMin.2-GFP-transfected targets cells were sorted by FACS and the population used in this experiment contained 60% fluorescent cells.

30 CTL stimulation was measured by quantitating the amount of IFN- γ release (A, B) or by lysis of ⁵¹Cr-labeled target cells (C, D, hatched bars). CTLs were stimulated with transfected cells (A, C) or with parental Jurkat-A2.1/K^b cells in the presence of 1 μ g/ml peptide (B, D). Levels of IFN- γ release and cytotoxicity for the different CTL lines in the absence of epitope ranged from 72-126 pg/ml and 2-6% respectively.

Figure 24. Summary of modified minigene constructs used to address variables critical for *in vivo* immunogenicity. The following modifications were incorporated into the prototype pMin.1 construct; A, deletion of PADRE HTL epitope; B, incorporation of the native HBV Pol 551 epitope that contains an alanine in position 9; C, 5 deletion of the Ig kappa signal sequence; and D, switching position of the HBV Env 335 and HBV Pol 455 epitopes.

Figure 25. Examination of variables that may influence pMin.1 immunogenicity. *In vivo* CTL-inducing activity of pMin.1 is compared to modified constructs. For ease of comparison, the CTL response induced by each of the modified 10 DNA minigene constructs (shaded bars) is compared separately in each of the four panels to the response induced by the prototype pMin.1 construct (solid bars). The geometric mean response of CTL-positive cultures from two to five independent experiments are shown. Numbers shown with each bar indicate the number of positive cultures/total number tested for that particular epitope. The ratio of positive cultures/total tested for the 15 pMin.1 group is shown in panel A and is the same for the remaining Figure panels (see Example V, Materials and Methods, *in vitro* CTL cultures, for the definition of a positive CTL culture). Theradigm responses were obtained by immunizing animals with the lipopeptide and stimulating and testing splenocyte cultures with the HBV Core 18-27 peptide.

20

DEFINITIONS

An "HTL" peptide epitope or an "MHC II epitope" is an MHC class II restricted epitope, i.e., one that is bound by an MHC class II molecule.

A "CTL" peptide epitope or an "MHC I epitope" is an MHC class I restricted epitope, i.e., one that is bound by an MHC class I molecule.

An "MHC targeting sequence" refers to a peptide sequence that targets a polypeptide, e.g., comprising a peptide epitope, to a cytosolic pathway (e.g., an MHC class I antigen processing pathway), an endoplasmic reticulum pathway, or an endocytic pathway (e.g., an MHC class II antigen processing pathway).

30 The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a

coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature, e.g., a fusion polypeptide comprising subsequence from different polypeptides, peptide epitopes from the same polypeptide that are not naturally in an adjacent position, or repeats of a single peptide epitope.

5 As used herein, the term “universal MHC class II epitope” or a “universal HTL epitope” refers to a MHC class II peptide epitope that binds to gene products of multiple MHC class II alleles. For example, the DR, DP and DQ alleles are human MHC II alleles. Generally, a unique set of peptides binds to a particular gene product of a MHC 10 class II allele. In contrast, a universal MHC class II epitope is able to bind to gene products of multiple MHC class II alleles. A universal MHC class II epitope binds to 2 or more MHC class II alleles, generally 3 or more MHC class II alleles, and particularly 5 or more MHC class II alleles. Thus, the presence of a universal MHC class II epitope in an expression vector is advantageous in that it functions to increase the number of allelic 15 MHC class II molecules that can bind to the peptide and, consequently, the number of Helper T lymphocytes that are activated.

Universal MHC class II epitopes are well known in the art and include, for example, epitopes such as the “pan DR epitopes,” also referred to as “PADRE” (Alexander *et al.*, *Immunity* 1:751-761 (1994); WO 95/07707, USSN 60/036,713, USSN 20 60/037,432, PCT/US98/01373, 09/009,953, and USSN 60/087,192 each of which is incorporated herein by reference). A “pan DR binding peptide” or a “PADRE” peptide of the invention is a peptide capable of binding at least about 7 different DR molecules, preferably 7 of the 12 most common DR molecules, most preferably 9 of the 12 most common DR molecules (DR1, 2w2b, 2w2a, 3, 4w4, 4w14, 5, 7, 52a, 52b, 52c, and 53), or alternatively, 50% of a panel of DR molecules representative of greater than or equal to 25 75% of the human population, preferably greater than or equal to 80% of the human population. Pan DR epitopes can bind to a number of DR alleles and are strongly immunogenic for T cells. For example, pan DR epitopes were found to be more effective at inducing an immune response than natural MHC class II epitopes (Alexander, *supra*). 30 An example of a PADRE epitope is the peptide AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38) (for additional examples of PADRE epitopes, see Table 8 of TTC docket No. 018623-006221, filed May 12, 1999, USSN _____, herein incorporated by reference in its entirety).

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC₅₀ (or K_D) of less than 50 nM. "Intermediate affinity" is binding with an IC₅₀ (or K_D) of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an K_D of less than 100 nM. "Intermediate affinity" is binding with a K_D of between about 100 and about 1000 nM. Assays for determining binding are described in detail, e.g., in PCT publications WO 94/20127 and WO 94/03205. Alternatively, binding is expressed relative to a reference peptide. As a particular assay becomes more, or less, sensitive, the IC₅₀s of the peptides tested may change somewhat. However, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide.

Throughout this disclosure, results are expressed in terms of "IC₅₀s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (i.e., limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (e.g., HLA preparation, etc.). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

The terms "identical" or percent "identity," in the context of two or more peptide sequences, refer to two or more sequences or subsequences that are the same or

have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithms using default program parameters or by manual alignment and visual inspection.

5 The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

10 "Major histocompatibility complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the HLA complex. For a detailed description of the MHC and HLA complexes, *see* Paul, *Fundamental Immunology* (3rd ed. 1993).

15 "Human leukocyte antigen" or "HLA" is a human class I or class II major histocompatibility complex (MHC) protein (*see, e.g.*, Stites, et al., *Immunology*, (8th ed., 1994)).

20 An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like supertype molecules (where xx denotes a particular HLA type), are synonyms.

25 The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

30 A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Thus, a preferably is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

 "Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing oligopeptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

An "immunogenic peptide" or "peptide epitope" is a peptide which 10 comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic peptide is derived.

A "protective immune response" refers to a CTL and/or an HTL response 15 to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic 20 incorporated into an oligopeptide by an amide bond or amide bond mimetic.

"Synthetic peptide" refers to a peptide that is not naturally occurring, but is man-made using such methods as chemical synthesis or recombinant DNA technology.

The nomenclature used to describe peptide compounds follows the 25 conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the 30 formulae representing selected specific embodiments of the present invention, the amino and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single

letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

As used herein, the term "expression vector" is intended to refer to a

- 5 nucleic acid molecule capable of expressing an antigen of interest such as a MHC class I or class II epitope in an appropriate target cell. An expression vector can be, for example, a plasmid or virus, including DNA or RNA viruses. The expression vector contains such a promoter element to express an antigen of interest in the appropriate cell or tissue in order to stimulate a desired immune response.

10

DETAILED DESCRIPTION OF THE INVENTION

- Cytotoxic T lymphocytes (CTLs) and helper T lymphocytes (HTLs) are critical for immunity against infectious pathogens; such as viruses, bacteria, and protozoa; tumor cells; autoimmune diseases and the like. The present invention provides 15 minigenes that encode peptide epitopes which induce a CTL and/or HTL response. The minigenes of the invention also include an MHC targeting sequence. A variety of minigenes encoding different epitopes can be tested for immunogenicity using an HLA transgenic mouse. The epitopes are typically a combination of at least two or more HTL epitopes, or a CTL epitope plus a universal HTL epitope, and optimally include additional 20 HTL and/or CTL epitopes. Two, three, four, five, six, seven, eight, nine, ten, twenty, thirty, forty or about fifty different epitopes, either HTL and/or CTL, can be included in the minigene, along with the MHC targeting sequence. The epitopes can have different HLA restriction. Epitopes to be tested include those derived from viruses such as HIV, HBV, HCV, HSV, CMV, HPV, and HTLV; cancer antigens such as p53, Her2/Neu, 25 MAGE, PSA, human papilloma virus, and CEA; parasites such as *Trypanosoma*, *Plasmodium*, *Leishmania*, *Giardia*, *Entamoeba*; autoimmune diseases such as rheumatoid arthritis, myesthenia gravis, and lupus erythematosus; fungi such as *Aspergillus* and *Candida*; and bacteria such as *Escherichia coli*, *Staphylococci*, *Chlamydia*, *Mycobacterium*, *Streptococci*, and *Pseudomonas*. The epitopes to be encoded by the minigene are selected 30 and tested using the methods described in published PCT applications WO 93/07421, WO 94/02353, WO 95/01000, WO 97/04451, and WO 97/05348, herein incorporated by reference.

HTL and CTL Epitopes

The expression vectors of the invention encode one or more MHC class II and/or class I epitopes and an MHC targeting sequence. Multiple MHC class II or class I epitopes present in an expression vector can be derived from the same antigen, or the 5 MHC epitopes can be derived from different antigens. For example, an expression vector can contain one or more MHC epitopes that can be derived from two different antigens of the same virus or from two different antigens of different viruses. Furthermore, any 10 MHC epitope can be used in the expression vectors of the invention. For example, any single MHC epitope or a combination of the MHC epitopes shown in Tables 1 to 8 can be used in the expression vectors of the invention. Other peptide epitopes can be selected by 15 one of skill in the art, e.g., by using a computer to select epitopes that contain HLA allele-specific motifs or supermotifs. The expression vectors of the invention can also encode one or more universal MHC class II epitopes, e.g., PADRE (see, e.g., SEQ ID NO:38 and Table 8 of TTC docket No. 018623-006221, filed May 12, 1999, USSN

15 _____).

Universal MHC class II epitopes can be advantageously combined with other MHC class I and class II epitopes to increase the number of cells that are activated in response to a given antigen and provide broader population coverage of MHC-reactive alleles. Thus, the expression vectors of the invention can encode MHC epitopes specific 20 for an antigen, universal MHC class II epitopes, or a combination of specific MHC epitopes and at least one universal MHC class II epitope.

MHC class I epitopes are generally about 5 to 15 amino acids in length, in particular about 8 to 11 amino acids in length. MHC class II epitopes are generally about 10 to 25 amino acids in length, in particular about 13 to 21 amino acids in length. A 25 MHC class I or II epitope can be derived from any desired antigen of interest. The antigen of interest can be a viral antigen, surface receptor, tumor antigen, oncogene, enzyme, or any pathogen, cell or molecule for which an immune response is desired. Epitopes can be selected based on their ability to bind one or multiple HLA alleles, and can also be selected using the "analog" technique described below.

30

Targeting Sequences

The expression vectors of the invention encode one or more MHC epitopes operably linked to a MHC targeting sequence. The use of a MHC targeting sequence enhances the immune response to an antigen, relative to delivery of antigen alone, by

directing the peptide epitope to the site of MHC molecule assembly and transport to the cell surface, thereby providing an increased number of MHC molecule-peptide epitope complexes available for binding to and activation of T cells.

- MHC class I targeting sequences are used in the present invention, e.g.,
- 5 those sequences that target an MHC class I epitope peptide to a cytosolic pathway or to the endoplasmic reticulum (*see, e.g.*, Rammensee *et al.*, *Immunogenetics* 41:178-228 (1995)). For example, the cytosolic pathway processes endogenous antigens that are expressed inside the cell. Although not wishing to be bound by any particular theory, cytosolic proteins are thought to be at least partially degraded by an endopeptidase
- 10 activity of a proteasome and then transported to the endoplasmic reticulum by the TAP molecule (transporter associated with processing). In the endoplasmic reticulum, the antigen binds to MHC class I molecules. Endoplasmic reticulum signal sequences bypass the cytosolic processing pathway and directly target endogenous antigens to the endoplasmic reticulum, where proteolytic degradation into peptide fragments occurs.
- 15 Such MHC class I targeting sequences are well known in the art, and include, e.g., signal sequences such as those from Ig kappa , tissue plasminogen activator or insulin. A preferred signal peptide is the human Ig kappa chain sequence. Endoplasmic reticulum signal sequences can also be used to target MHC class II epitopes to the endoplasmic reticulum, the site of MHC class I molecule assembly.
- 20 MHC class II targeting sequences are also used in the invention, e.g., those that target a peptide to the endocytic pathway. These targeting sequences typically direct extracellular antigens to enter the endocytic pathway, which results in the antigen being transferred to the lysosomal compartment where the antigen is proteolytically cleaved into antigen peptides for binding to MHC class II molecules. As with the normal
- 25 processing of exogenous antigen, a sequence that directs a MHC class II epitope to the endosomes of the endocytic pathway and/or subsequently to lysosomes, where the MHC class II epitope can bind to a MHC class II molecule, is a MHC class II targeting sequence. For example, group of MHC class II targeting sequences useful in the invention are lysosomal targeting sequences, which localize polypeptides to lysosomes.
- 30 Since MHC class II molecules typically bind to antigen peptides derived from proteolytic processing of endocytosed antigens in lysosomes, a lysosomal targeting sequence can function as a MHC class II targeting sequence. Lysosomal targeting sequences are well known in the art and include sequences found in the lysosomal proteins LAMP-1 and

LAMP-2 as described by August *et al.* (U.S. Patent No. 5,633,234, issued May 27, 1997), which is incorporated herein by reference.

Other lysosomal proteins that contain lysosomal targeting sequences include HLA-DM. HLA-DM is an endosomal/lysosomal protein that functions in facilitating binding of antigen peptides to MHC class II molecules. Since it is located in the lysosome, HLA-DM has a lysosomal targeting sequence that can function as a MHC class II molecule targeting sequence (Copier *et al.*, *J. Immunol.* 157:1017-1027 (1996), which is incorporated herein by reference).

The resident lysosomal protein HLA-DO can also function as a lysosomal targeting sequence. In contrast to the above described resident lysosomal proteins LAMP-1 and HLA-DM, which encode specific Tyr-containing motifs that target proteins to lysosomes, HLA-DO is targeted to lysosomes by association with HLA-DM (Liljedahl *et al.*, *EMBO J.* 15:4817-4824 (1996)), which is incorporated herein by reference. Therefore, the sequences of HLA-DO that cause association with HLA-DM and, consequently, translocation of HLA-DO to lysosomes can be used as MHC class II targeting sequences. Similarly, the murine homolog of HLA-DO, H2-DO, can be used to derive a MHC class II targeting sequence. A MHC class II epitope can be fused to HLA-DO or H2-DO and targeted to lysosomes.

In another example, the cytoplasmic domains of B cell receptor subunits Ig- α and Ig- β mediate antigen internalization and increase the efficiency of antigen presentation (Bonnerot *et al.*, *Immunity* 3:335-347 (1995)), which is incorporated herein by reference. Therefore, the cytoplasmic domains of the Ig- α and Ig- β proteins can function as MHC class II targeting sequences that target a MHC class II epitope to the endocytic pathway for processing and binding to MHC class II molecules.

Another example of a MHC class II targeting sequence that directs MHC class II epitopes to the endocytic pathway is a sequence that directs polypeptides to be secreted, where the polypeptide can enter the endosomal pathway. These MHC class II targeting sequences that direct polypeptides to be secreted mimic the normal pathway by which exogenous, extracellular antigens are processed into peptides that bind to MHC class II molecules. Any signal sequence that functions to direct a polypeptide through the endoplasmic reticulum and ultimately to be secreted can function as a MHC class II targeting sequence so long as the secreted polypeptide can enter the endosomal/lysosomal pathway and be cleaved into peptides that can bind to MHC class II molecules. An

example of such a fusion is shown in Figure 11, where the signal sequence of kappa immunoglobulin is fused to multiple MHC class II epitopes.

In another example, the Ii protein binds to MHC class II molecules in the endoplasmic reticulum, where it functions to prevent peptides present in the endoplasmic reticulum from binding to the MHC class II molecules. Therefore, fusion of a MHC class II epitope to the Ii protein targets the MHC class II epitope to the endoplasmic reticulum and a MHC class II molecule. For example, the CLIP sequence of the Ii protein can be removed and replaced with a MHC class II epitope sequence so that the MHC class II epitope is directed to the endoplasmic reticulum, where the epitope binds to a MHC class II molecule.

In some cases, antigens themselves can serve as MHC class II or I targeting sequences and can be fused to a universal MHC class II epitope to stimulate an immune response. Although cytoplasmic viral antigens are generally processed and presented as complexes with MHC class I molecules, long-lived cytoplasmic proteins such as the influenza matrix protein can enter the MHC class II molecule processing pathway (Guéguen & Long, *Proc. Natl. Acad. Sci. USA* 93:14692-14697 (1996)), which is incorporated herein by reference. Therefore, long-lived cytoplasmic proteins can function as a MHC class II targeting sequence. For example, an expression vector encoding influenza matrix protein fused to a universal MHC class II epitope can be advantageously used to target influenza antigen and the universal MHC class II epitope to the MHC class II pathway for stimulating an immune response to influenza.

Other examples of antigens functioning as MHC class II targeting sequences include polypeptides that spontaneously form particles. The polypeptides are secreted from the cell that produces them and spontaneously form particles, which are taken up into an antigen-presenting cell by endocytosis such as receptor-mediated endocytosis or are engulfed by phagocytosis. The particles are proteolytically cleaved into antigen peptides after entering the endosomal/lysosomal pathway.

One such polypeptide that spontaneously forms particles is HBV surface antigen (HBV-S) (Diminsky *et al.*, *Vaccine* 15:637-647 (1997); Le Borgne *et al.*, *Virology* 240:304-315 (1998)), each of which is incorporated herein by reference. Another polypeptide that spontaneously forms particles is HBV core antigen (Kuhröber *et al.*, *International Immunol.* 9:1203-1212 (1997)), which is incorporated herein by reference. Still another polypeptide that spontaneously forms particles is the yeast Ty protein (Weber *et al.*, *Vaccine* 13:831-834 (1995)), which is incorporated herein by

reference. For example, an expression vector containing HBV-S antigen fused to a universal MHC class II epitope can be advantageously used to target HBV-S antigen and the universal MHC class II epitope to the MHC class II pathway for stimulating an immune response to HBV.

5

Binding Affinity of Peptide Epitopes for HLA Molecules

The large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at 10 high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have a binding affinity for class I HLA molecules of less than 500 nM. 15 HTL-inducing peptides preferably include those that have a binding affinity for class II HLA molecules of less than 1000 nM. For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred 20 embodiments, peptides that exhibit cross-reactive binding are then used in vaccines or in cellular screening analyses.

Higher HLA binding affinity is typically correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the 25 vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides leads to more vigorous immunogenic 30 responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (Sette *et al.*, 5 *J. Immunol.* 153:5586-5592 (1994)). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL (peripheral blood 10 lymphocytes) from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for 15 synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g.*, Schaeffer *et al.* *Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.*, Southwood *et al.* *J. Immunology* 160:3363-3373 (1998), and USSN 60/087192, filed 5/29/98). In order to 20 define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (i.e., the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, i.e. binding affinities of less than 100 nM. In the other half of the cases (16 of 32), DR restriction was 25 associated with intermediate affinity (binding affinities in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC₅₀ of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

30 Peptide Epitope Binding Motifs and Supermotifs

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets.

For HLA molecule pocket analyses, the residues comprising the B and F pockets of HLA class I molecules as described in crystallographic studies were analyzed (Guo *et al.*, *Nature* 360:364 (1992); Saper *et al.*, *J. Mol. Biol.* 219:277 (1991); Madden *et al.*, *Cell* 75:693 (1993); Parham *et al.*, *Immunol. Rev.* 143:141 (1995)). In these analyses, 5 residues 9, 45, 63, 66, 67, 70, and 99 were considered to make up the B pocket; and the B pocket was deemed to determine the specificity for the amino acid residue in the second position of peptide ligands. Similarly, residues 77, 80, 81, and 116 were considered to determine the specificity of the F pocket; the F pocket was deemed to determine the specificity for the C-terminal residue of a peptide ligand bound by the HLA class I 10 molecule.

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification 15 of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912 (1994)) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and 20 overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value 25 of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecules with high or intermediate affinity. Of these 22 peptides, 20, (i.e., 91%), were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques eliminates screening of 90% of the potential epitopes in a target antigen protein sequence.

30 Peptides of the present invention may also include epitopes that bind to MHC class II DR molecules. There is a significant difference between class I and class II HLA molecules. This difference corresponds to the fact that, although a stringent size restriction and motif position relative to the binding pocket exists for peptides that bind to class I molecules, a greater degree of heterogeneity in both size and binding frame

position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands.

This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the residues occupying position 1 and position 6 of peptides complexed with DRB*0101 engage two complementary pockets on the DRBa*0101 molecules, with the P1 position corresponding to the most crucial anchor residue and the deepest hydrophobic pocket (see, e.g., Madden, *Ann. Rev. Immunol.* 10: 13.587 (1995)). Other studies have also pointed to the P6 position as a crucial anchor residue for binding to various other DR molecules.

Thus, peptides of the present invention are identified by any one of several HLA class I or II -specific amino acid motifs (see, e.g., Tables I-III of USSN 09/226,775, and 09/239,043, herein incorporated by reference in their entirety). If the presence of the motif corresponds to the ability to bind several allele-specific HLA antigens it is referred to as a supermotif. The allele-specific HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel *et al.*, *Adv. Immunol.* 27:5159 (1979); Bennink *et al.*, *J. Exp. Med.* 168:1935-1939 (1988); Rawle *et al.*, *J. Immunol.* 146:3977-3984 (1991)). It has been recognized that immunodominance (Benacerraf *et al.*, *Science* 175:273-279 (1972)) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello *et al.*, *J. Immunol.* 131:1635 (1983)); Rosenthal *et al.*, *Nature* 267:156-158 (1977)), or being selectively recognized by the existing TCR (T cell receptor) specificity (repertoire theory) (Klein, *Immunology, The Science of Self on self Discrimination*, pp. 270-310 (1982)). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz *et al.*, *Annu. Rev. Immunol.* 11:729-766 (1993)).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities
5 have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco *et al.*, *Curr. Opin. Immunol.* 7:524-531 (1995)). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or
10 prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC₅₀ in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL
15 bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC₅₀ of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette *et al.*, *J. Immunol.*, 153:558-5592 (1994)). In the cancer setting this phenomenon is probably due to elimination, or functional inhibition of the CTL recognizing several of the highest binding
20 peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow extant T cells to be recruited, which will then lead to a therapeutic or prophylactic response. However, the binding of HLA molecules to subdominant epitopes
25 is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide-based vaccines and therapeutic agents.

30 Thus, although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to further increase cross-reactivity of peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability.

Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (i.e., analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding capacity can be performed. More specifically, peptides which exhibit the
5 broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending USSN 09/226,775.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate with binding to certain HLA class I and II molecules. The motifs or supermotifs
10 are defined by having primary anchors, and in many cases secondary anchors (see Tables I-III of USSN 09/226,775). Analog peptides can be created by substituting amino acids residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and motifs that have
15 been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively, of USSN 09/226,775.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind to the respective motif or supermotif
20 (see Tables II and III of USSN 09/226,775). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the methods described therein. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of analyzed peptides, the incidence of cross-reactivity increases from 22% to 37% (I., Sidney *et al.*, *Hu. Immunol.* 45:79
25 (1996)). Thus, one strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with elimination of detrimental residues within a peptide, "preferred" residues
30 associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, a failure to elicit helper T cells that cross-react with the wild type peptides), the analog peptide may

be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. In both class I and class II systems it will be desirable to use as targets, cells that have been either infected or transfected with the appropriate genes to 5 establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I peptides exhibiting binding affinities of 500-50000 nM, and carrying an acceptable but 10 suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in, 15 e.g., a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of gamma-amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting gamma-amino butyric acid for C not only alleviates this problem, but 20 actually improves binding and crossbinding capability in certain instances (Sette *et al*, *In: Persistent Viral Infections* (Ahmed & Chen, eds., 1998)). Substitution of cysteine with gamma-amino butyric acid may occur at any residue of a peptide epitope, i.e., at either anchor or non-anchor positions.

25 Expression Vectors and Construction of a Minigene

The expression vectors of the invention contain at least one promoter element that is capable of expressing a transcription unit encoding the antigen of interest, for example, a MHC class I epitope or a MHC class II epitope and an MHC targeting sequence in the appropriate cells of an organism so that the antigen is expressed and 30 targeted to the appropriate MHC molecule. For example, if the expression vector is administered to a mammal such as a human, a promoter element that functions in a human cell is incorporated into the expression vector. An example of an expression vector useful for expressing the MHC class II epitopes fused to MHC class II targeting

sequences and the MHC class I epitopes described herein is the pEP2 vector described in Example IV.

This invention relies on routine techniques in the field of recombinant genetics. Basic texts disclosing the general methods of use in this invention include 5 Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds., 1994); *Oligonucleotide Synthesis: A Practical Approach* (Gait, ed., 1984); Kuijpers, *Nucleic Acids Research* 18(17):5197 (1994); Dueholm, *J. Org. Chem.* 59:5767-5773 (1994); *Methods in Molecular Biology*, volume 10 20 (Agrawal, ed.); and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, e.g., Part I, chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" (1993)).

The minigenes are comprised of two or many different epitopes (see, e.g., Tables 1-8). The nucleic acid encoding the epitopes are assembled in a minigene 15 according to standard techniques. In general, the nucleic acid sequences encoding minigene epitopes are isolated using amplification techniques with oligonucleotide primers, or are chemically synthesized. Recombinant cloning techniques can also be used when appropriate. Oligonucleotide sequences are selected which either amplify (when using PCR to assemble the minigene) or encode (when using synthetic oligonucleotides to 20 assemble the minigene) the desired epitopes.

Amplification techniques using primers are typically used to amplify and isolate sequences encoding the epitopes of choice from DNA or RNA (see U.S. Patents 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis *et al.*, eds, 1990)). Methods such as polymerase chain reaction (PCR) and ligase chain 25 reaction (LCR) can be used to amplify epitope nucleic acid sequences directly from mRNA, from cDNA, from genomic libraries or cDNA libraries. Restriction endonuclease sites can be incorporated into the primers. Minigenes amplified by the PCR reaction can be purified from agarose gels and cloned into an appropriate vector.

Synthetic oligonucleotides can also be used to construct minigenes. This 30 method is performed using a series of overlapping oligonucleotides, representing both the sense and non-sense strands of the gene. These DNA fragments are then annealed, ligated and cloned. Oligonucleotides that are not commercially available can be chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage & Caruthers, *Tetrahedron Letts.* 22:1859-1862 (1981), using an

automated synthesizer, as described in Van Devanter *et. al.*, *Nucleic Acids Res.* 12:6159-6168 (1984). Purification of oligonucleotides is by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson & Reanier, *J. Chrom.* 255:137-149 (1983).

5 The epitopes of the minigene are typically subcloned into an expression vector that contains a strong promoter to direct transcription, as well as other regulatory sequences such as enhancers and polyadenylation sites. Suitable promoters are well known in the art and described, e.g., in Sambrook *et al.* and Ausubel *et al.* Eukaryotic expression systems for mammalian cells are well known in the art and are commercially 10 available. Such promoter elements include, for example, cytomegalovirus (CMV), Rous sarcoma virus LTR and SV40.

15 The expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the minigene in host cells. A typical expression cassette thus contains a promoter operably linked to the minigene and signals required for efficient polyadenylation of the transcript. Additional elements of the cassette may include enhancers and introns with functional 20 splice donor and acceptor sites.

25 In addition to a promoter sequence, the expression cassette can also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from different genes.

30 The particular expression vector used to transport the genetic information into the cell is not particularly critical. Any of the conventional vectors used for expression in eukaryotic cells may be used. Expression vectors containing regulatory elements from eukaryotic viruses are typically used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, and vectors derived from Epstein Bar virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A+, pMTO10/A+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the SV40 early promoter, SV40 later promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells. In one embodiment, the vector pEP2 is used in the present invention.

Other elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit

selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of eukaryotic sequences. The particular antibiotic resistance gene chosen is not critical, any of the many resistance genes known in the art are suitable. The prokaryotic sequences are preferably chosen such that they do not interfere with the replication of the DNA in eukaryotic cells, if necessary.

Administration In Vivo

The invention also provides methods for stimulating an immune response by administering an expression vector of the invention to an individual. Administration of an expression vector of the invention for stimulating an immune response is advantageous because the expression vectors of the invention target MHC epitopes to MHC molecules, thus increasing the number of CTL and HTL activated by the antigens encoded by the expression vector.

Initially, the expression vectors of the invention are screened in mouse to determine the expression vectors having optimal activity in stimulating a desired immune response. Initial studies are therefore carried out, where possible, with mouse genes of the MHC targeting sequences. Methods of determining the activity of the expression vectors of the invention are well known in the art and include, for example, the uptake of ^{3}H -thymidine to measure T cell activation and the release of ^{51}Cr to measure CTL activity as described below in Examples II and III. Experiments similar to those described in Example IV are performed to determine the expression vectors having activity at stimulating an immune response. The expression vectors having activity are further tested in human. To circumvent potential adverse immunological responses to encoded mouse sequences, the expression vectors having activity are modified so that the MHC class II targeting sequences are derived from human genes. For example, substitution of the analogous regions of the human homologs of genes containing various MHC class II targeting sequences are substituted into the expression vectors of the invention. Examples of such human homologs of genes containing MHC class II targeting sequences are shown in Figures 12 to 17. Expression vectors containing human MHC class II targeting sequences, such as those described in Example I below, are tested for activity at stimulating an immune response in human.

The invention also relates to pharmaceutical compositions comprising a pharmaceutically acceptable carrier and an expression vector of the invention.

Pharmaceutically acceptable carriers are well known in the art and include aqueous or non-aqueous solutions, suspensions and emulsions, including physiologically buffered saline, alcohol/aqueous solutions or other solvents or vehicles such as glycols, glycerol, oils such as olive oil or injectable organic esters.

5 A pharmaceutically acceptable carrier can contain physiologically acceptable compounds that act, for example, to stabilize the expression vector or increase the absorption of the expression vector. Such physiologically acceptable compounds include, for example, carbohydrates, such as glucose, sucrose or dextrans, antioxidants such as ascorbic acid or glutathione, chelating agents, low molecular weight polypeptides, 10 antimicrobial agents, inert gases or other stabilizers or excipients. Expression vectors can additionally be complexed with other components such as peptides, polypeptides and carbohydrates. Expression vectors can also be complexed to particles or beads that can be administered to an individual, for example, using a vaccine gun. One skilled in the art would know that the choice of a pharmaceutically acceptable carrier, including a 15 physiologically acceptable compound, depends, for example, on the route of administration of the expression vector.

The invention further relates to methods of administering a pharmaceutical composition comprising an expression vector of the invention to stimulate an immune response. The expression vectors are administered by methods well known in the art as 20 described in Donnelly *et al.* (*Ann. Rev. Immunol.* 15:617-648 (1997)); Felgner *et al.* (U.S. Patent No. 5,580,859, issued December 3, 1996); Felgner (U.S. Patent No. 5,703,055, issued December 30, 1997); and Carson *et al.* (U.S. Patent No. 5,679,647, issued October 21, 1997), each of which is incorporated herein by reference. In one embodiment, the minigene is administered as naked nucleic acid.

25 A pharmaceutical composition comprising an expression vector of the invention can be administered to stimulate an immune response in a subject by various routes including, for example, orally, intravaginally, rectally, or parenterally, such as intravenously, intramuscularly, subcutaneously, intraorbitally, intracapsularly, intraperitoneally, intracisternally or by passive or facilitated absorption through the skin 30 using, for example, a skin patch or transdermal iontophoresis, respectively. Furthermore, the composition can be administered by injection, intubation or topically, the latter of which can be passive, for example, by direct application of an ointment or powder, or active, for example, using a nasal spray or inhalant. An expression vector also can be administered as a topical spray, in which case one component of the composition is an

appropriate propellant. The pharmaceutical composition also can be incorporated, if desired, into liposomes, microspheres or other polymer matrices (Felgner *et al.*, U.S. Patent No. 5,703,055; Gregoriadis, *Liposome Technology*, Vols. I to III (2nd ed. 1993), each of which is incorporated herein by reference). Liposomes, for example, which consist of phospholipids or other lipids, are nontoxic, physiologically acceptable and metabolizable carriers that are relatively simple to make and administer.

The expression vectors of the invention can be delivered to the interstitial spaces of tissues of an animal body (Felgner *et al.*, U.S. Patent Nos. 5,580,859 and 5,703,055). Administration of expression vectors of the invention to muscle is a particularly effective method of administration, including intradermal and subcutaneous injections and transdermal administration. Transdermal administration, such as by iontophoresis, is also an effective method to deliver expression vectors of the invention to muscle. Epidermal administration of expression vectors of the invention can also be employed. Epidermal administration involves mechanically or chemically irritating the outermost layer of epidermis to stimulate an immune response to the irritant (Carson *et al.*, U.S. Patent No. 5,679,647).

Other effective methods of administering an expression vector of the invention to stimulate an immune response include mucosal administration (Carson *et al.*, U.S. Patent No. 5,679,647). For mucosal administration, the most effective method of administration includes intranasal administration of an appropriate aerosol containing the expression vector and a pharmaceutical composition. Suppositories and topical preparations are also effective for delivery of expression vectors to mucosal tissues of genital, vaginal and ocular sites. Additionally, expression vectors can be complexed to particles and administered by a vaccine gun.

The dosage to be administered is dependent on the method of administration and will generally be between about 0.1 µg up to about 200 µg. For example, the dosage can be from about 0.05 µg/kg to about 50 mg/kg, in particular about 0.005-5 mg/kg. An effective dose can be determined, for example, by measuring the immune response after administration of an expression vector. For example, the production of antibodies specific for the MHC class II epitopes or MHC class I epitopes encoded by the expression vector can be measured by methods well known in the art, including ELISA or other immunological assays. In addition, the activation of T helper cells or a CTL response can be measured by methods well known in the art including, for

example, the uptake of ^3H -thymidine to measure T cell activation and the release of ^{51}Cr to measure CTL activity (*see Examples II and III below*).

The pharmaceutical compositions comprising an expression vector of the invention can be administered to mammals, particularly humans, for prophylactic or therapeutic purposes. Examples of diseases that can be treated or prevented using the expression vectors of the invention include infection with HBV, HCV, HIV and CMV as well as prostate cancer, renal carcinoma, cervical carcinoma, lymphoma, condyloma acuminatum and acquired immunodeficiency syndrome (AIDS).

In therapeutic applications, the expression vectors of the invention are administered to an individual already suffering from cancer, autoimmune disease or infected with a virus. Those in the incubation phase or acute phase of the disease can be treated with expression vectors of the invention, including those expressing all universal MHC class II epitopes, separately or in conjunction with other treatments, as appropriate.

In therapeutic and prophylactic applications, pharmaceutical compositions comprising expression vectors of the invention are administered to a patient in an amount sufficient to elicit an effective immune response to an antigen and to ameliorate the signs or symptoms of a disease. The amount of expression vector to administer that is sufficient to ameliorate the signs or symptoms of a disease is termed a therapeutically effective dose. The amount of expression vector sufficient to achieve a therapeutically effective dose will depend on the pharmaceutical composition comprising an expression vector of the invention, the manner of administration, the state and severity of the disease being treated, the weight and general state of health of the patient and the judgment of the prescribing physician.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

EXAMPLES

The following example is provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

5

EXAMPLE I: Construction of Expression Vectors Containing MHC Class II Epitopes

This example shows construction of expression vectors containing MHC class II epitopes that can be used to target antigens to MHC class II molecules.

Expression vectors comprising DNA constructs were prepared using 10 overlapping oligonucleotides, polymerase chain reaction (PCR) and standard molecular biology techniques (Dieffenbach & Dveksler, *PCR Primer: A Laboratory Manual* (1995); Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (2nd ed., 1989), each of which is incorporated herein by reference).

To generate full length wild type Ii, the full length invariant chain was 15 amplified, cloned, and sequenced and used in the construction of the three invariant chain constructs. Except where noted, the source of cDNA for all the constructs listed below was Mouse Spleen Marathon-Ready cDNA made from Balb/c males (Clontech; Palo Alto CA). The primer pairs were the oligonucleotide
GCTAGCGCCGCCACCATGGATGACCAACGCGACCTC (SEQ ID NO:40), which is 20 designated murIi-F and contains an NheI site followed by the consensus Kozak sequence and the 5' end of the Ii cDNA; and the oligonucleotide
GGTACCTCACAGGGTGACTTGACCCAG (SEQ ID NO:41), which is designated murIi-R and contains a KpnI site and the 3' end of the Ii coding sequence.

For the PCR reaction, 5 µl of spleen cDNA and 250 nM of each primer 25 were combined in a 100 µl reaction with 0.25 mM each dNTP and 2.5 units of *Pfu* polymerase in *Pfu* polymerase buffer containing 10 mM KCl, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% TRITON X-100 and 100 µg/ml bovine serum albumin (BSA). A Perkin/Elmer 9600 PCR machine (Perkin Elmer; Foster City CA) was used and the cycling conditions were: 1 cycle of 95°C for 5 minutes, followed by 30 cycles of 95°C for 15 seconds, 52°C for 30 seconds, and 72°C for 1 minute. The PCR reaction was run on a 1% agarose gel, and the 670 base pair product was cut out, purified by spinning through a Millipore Ultrafree-MC filter (Millipore; Bedford MA) and cloned into pCR-Blunt from Invitrogen (San Diego, CA). Individual clones were screened by

sequencing, and a correct clone (named bIi#3) was used as a template for the helper constructs.

DNA constructs containing pan DR epitope sequences and MHC II targeting sequences derived from the Ii protein were prepared. The Ii murine protein has been previously described (Zhu & Jones, *Nucleic Acids Res.* 17:447-448 (1989)), which is incorporated herein by reference. Briefly, the IiPADRE construct contains the full length Ii sequence with PADRE precisely replacing the CLIP region. The DNA construct encodes amino acids 1 through 87 of invariant chain, followed with the 13 amino acid PADRE sequence (SEQ ID NO:38) and the rest of the invariant chain DNA sequence (amino acids 101-215). The construct was amplified in 2 overlapping halves that were joined to produce the final construct. The two primers used to amplify the 5' half were murIi-F and the oligonucleotide CAGGGTCCAGGCAGCCACGAACCTGGCCACAGGTTGGCAGA (SEQ ID NO:42), which is designated IiPADRE-R. The IiPADRE-R primer includes nucleotides 303-262 of IiPADRE. The 3' half was amplified with the primer GGCTGCCTGGACCCTGAAGGCTGCCGCTATGTCCATGGATAAC (SEQ ID NO:43), which is designated IiPADRE-F and includes nucleotides 288-330 of IiPADRE; and murIi-R. The PCR conditions were the same as described above, and the two halves were isolated by agarose gel electrophoresis as described above.

Ten microliters of each PCR product was combined in a 100 µl PCR reaction with an annealing temperature of 50°C for five cycles to generate a full length template. Primers murIi-F and murIi-R were added and 25 more cycles carried out. The full length IiPADRE product was isolated, cloned, and sequenced as described above. This construct contains the murine Ii gene with a pan DR epitope sequence substituted for the CLIP sequence of Ii (Figure 1).

A DNA construct, designated I80T, containing the cytoplasmic domain, the transmembrane domain and part of the luminal domain of Ii fused to a string of multiple MHC class II epitopes was constructed (Figure 2). Briefly, the string of multiple MHC class II epitopes was constructed with three overlapping oligonucleotides (oligos). Each oligo overlapped its neighbor by 15 nucleotides and the final MHC class II epitope string was assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. The three oligonucleotides were: oligo 1, nucleotides 241-310, CTTCGCATGAAGCTTATCAGCCAGGCTGTGCACGCCGCTCACGCCGAAATCAA CGAAGCTGGAAGAACCC (SEQ ID NO:44);

oligo 2, nucleotides 364-295,
TTCTGGTCAGCAGAAAGAACAGGATAGGAGCGTTGGAGGGCGATAAGCTGG
AGGGGTTCTTCCAGCTTC (SEQ ID NO:45); and

- oligo 3, nucleotides 350-42,
5 TTCTGCTGACCAGAACATCCTGACAATCCCCAGTCCCTGGACGCCAAGTCGTG
GCTGCCTGGACCCTGAAG (SEQ ID NO:46).

For the first PCR reaction, 5 µg of oligos 1 and 2 were combined in a 100 µl reaction containing *Pfu* polymerase. A Perkin/Elmer 9600 PCR machine was used and the annealing temperature used was 45° C. The PCR product was gel-purified, and a 10 second reaction containing the PCR product of oligos 1 and 2 with oligo 3 was annealed and extended for 10 cycles before gel purification of the full length product to be used as a "mega-primer."

The I80T construct was made by amplifying bIi#3 with murIi-F and the mega-primer. The cycling conditions were: 1 cycle of 95° C for 5 minutes, followed by 5 15 cycles of 95° C for 15 seconds, 37° C for 30 seconds, and 72° C for 1 minute. Primer Help-epR was added and an additional 25 cycles were carried out with the annealing temperature raised to 47° C. The Help-epR primer
GGTACCTCAAGCGGCAGCCTCAGGGTCCAGGCA (SEQ ID NO:47) corresponds to nucleotides 438-405. The full length I80T product was isolated, cloned, and sequenced 20 as above.

- The I80T construct (Figure 2) encodes amino acid residues 1 through 80 of Ii, containing the cytoplasmic domain, the transmembrane domain and part of the luminal domain, fused to a string of multiple MHC class II epitopes corresponding to: amino acid residues 323-339 of ovalbumin
25 (IleSerGlnAlaValHisAlaAlaHisAlaGluIleAsnGluAlaGlyArg; SEQ ID NO:48); amino acid residues 128 to 141 of HBV core antigen (amino acids ThrProProAlaTyrArgProProAsnAlaProIleLeu; SEQ ID NO:49); amino acid residues 182 to 196 of HBV env (amino acids PhePheLeuLeuThrArgIleLeuThrIleProGlnSerLeuAsp; SEQ ID NO:50); and the pan DR sequence designated SEQ ID NO:38.

30 A DNA construct containing the cytoplasmic domain, transmembrane domain and a portion of the luminal domain of Ii fused to the MHC class II epitope string shown in Figure 2 and amino acid residues 101 to 215 of Ii encoding the trimerization region of Ii was generated (Figure 3). This construct, designated IiThfull, encodes the first 80 amino acids of invariant chain followed by the MHC class II epitope string

(replacing CLIP) and the rest of the invariant chain (amino acids 101-215). Briefly, the construct was generated as two overlapping halves that were annealed and extended by PCR to yield the final product.

The 5' end of IiThfull was made by amplifying I80T with murIi-F (SEQ ID NO:40) and Th-Pad-R. The Th-Pad-R primer AGCGGCAGCCTTCAGGGTC (SEQ ID NO:51) corresponds to nucleotides 429-411. The 3' half was made by amplifying bIi#3 with IiPADRE-F and murIi-R (SEQ ID NO:41). The IiPADRE-F primer GGCTGCCTGGACCCTGAAGGCTGCCGCTATGTCCATGGATAAC (SEQ ID NO:52) corresponds to nucleotides 402-444. Each PCR product was gel purified and mixed, then denatured, annealed, and extended by five cycles of PCR. Primers murIi-F (SEQ ID NO:40) and murIi-R (SEQ ID NO:41) were added and another 25 cycles performed. The full length product was gel purified, cloned, and sequenced.

All of the remaining constructs described below were made essentially according to the scheme shown in Figure 18. Briefly, primer pairs 1F plus 1R, designated below for each specific construct, were used to amplify the specific signal sequence and contained an overlapping 15 base pair tail identical to the 5' end of the MHC class II epitope string. Primer pair Th-ova-F, ATCAGCCAGGCTGTGCACGC (SEQ ID NO:53), plus Th-Pad-R (SEQ ID NO:51) were used to amplify the MHC class II epitope string. A 15 base pair overlap and the specific transmembrane and cytoplasmic tail containing the targeting signals were amplified with primer pairs 2F plus 2R.

All three pieces of each cDNA were amplified using the following conditions: 1 cycle of 95°C for 5 minutes, followed by 30 cycles of 95°C for 15 seconds, 52°C for 30 seconds, and 72°C for 1 minute. Each of the three fragments was agrose-gel purified, and the signal sequence and MHC class II string fragments were combined and joined by five cycles in a second PCR. After five cycles, primers 1F and Th-Pad-R were added for 25 additional cycles and the PCR product was gel purified. This signal sequence plus MHC class II epitope string fragment was combined with the transmembrane plus cytoplasmic tail fragment for the final PCR. After five cycles, primers 1F plus 2R were added for 25 additional cycles and the product was gel purified, cloned and sequenced.

A DNA construct containing the murine immunoglobulin kappa signal sequence fused to the T helper epitope string shown in Figure 2 and the transmembrane and cytoplasmic domains of LAMP-1 was generated (Figure 4) (Granger *et al.*, *J. Biol. Chem.* 265:12036-12043 (1990)), which is incorporated by reference (mouse LAMP-1

GenBank accession No. M32015). This construct, designated kappaLAMP-Th, contains the consensus mouse immunoglobulin kappa signal sequence and was amplified from a plasmid containing full length immunoglobulin kappa as depicted in Figure 18. The primer 1F used was the oligonucleotide designated KappaSig-F,

5 GCTAGCGCCGCCACCATGGGAATGCAG (SEQ ID NO:54).

The primer 1R used was the oligonucleotide designated Kappa-Th-R,
CACAGCCTGGCTGATTCTCTGGACCC (SEQ ID NO:55).

The primer 2F used was the oligonucleotide designated PAD/LAMP-F,
CTGAAGGCTGCCGCTAACACATGTTGATCCCC (SEQ ID NO:56). The primer 2R
10 used was the oligonucleotide designated LAMP-CYTOR,
GGTACCCTAGATGGTCTGATAGCC (SEQ ID NO:57).

A DNA construct containing the signal sequence of H2-M fused to the
MHC class II epitope string shown in Figure 2 and the transmembrane and cytoplasmic
domains of H2-M was generated (Figure 5). The mouse H2-M gene has been described
15 previously, Peleraux *et al.*, *Immunogenetics* 43:204-214 (1996)), which is incorporated
herein by reference. This construct was designated H2M-Th and was constructed as
depicted in Figure 18. The primer 1F used was the oligonucleotide designated H2-Mb-
1F, GCC GCT AGC GCC ACC ATG GCT GCA CTC TGG (SEQ ID NO:58). The
primer 1R used was the oligonucleotide designated H2-Mb-1R, CAC AGC CTG GCT
20 GAT CCC CAT ACA GTG CAG (SEQ ID NO:59). The primer 2F used was the
oligonucleotide designated H2-Mb-2F, CTG AAG GCT GCC GCT AAG GTC TCT GTG
TCT (SEQ ID NO:60). The primer 2R used was the oligonucleotide designated H2-Mb-
2R, GCG GGT ACC CTA ATG CCG TCC TTC (SEQ ID NO:61).

A DNA construct containing the signal sequence of H2-DO fused to the
25 MHC class II epitope string shown in Figure 2 and the transmembrane and cytoplasmic
domains of H2-DO was generated (Figure 6). The mouse H2-DO gene has been
described previously (Larhammar *et al.*, *J. Biol. Chem.* 260:14111-14119 (1985)), which
is incorporated herein by reference (GenBank accession No. M19423). This construct,
designated H2O-Th, was constructed as depicted in Figure 18. The primer 1F used was
30 the oligonucleotide designated H2-Ob-1F, GCG GCT AGC GCC ACC ATG GGC
GCT GGG AGG (SEQ ID NO:62). The primer 1R used was the oligonucleotide
designated H2-Ob-1R, TGC ACA GCC TGG CTG ATG GAA TCC AGC CTC (SEQ ID
NO:63). The primer 2F used was the oligonucleotide designated H2-Ob-2F, CTG AAG
GCT GCC GCT ATA CTG AGT GGA GCT (SEQ ID NO:64). The primer 2R used was

the oligonucleotide designated H2-Ob-2R, GCC GGT ACC TCA TGT GAC ATG TCC CG (SEQ ID NO:65).

A DNA construct containing a pan DR epitope sequence (SEQ ID NO:38) fused to the amino-terminus of influenza matrix protein is generated (Figure 7). This 5 construct, designated PADRE-Influenza matrix, contains the universal MHC class II epitope PADRE attached to the amino terminus of the influenza matrix coding sequence. The construct is made using a long primer on the 5' end primer. The 5' primer is the oligonucleotide

GCTAGCGCCGCCACCATGGCCAAGTCGTGGCTGCCTGGACCCCTGAAGGGCTGC
10 CGCTATGAGTCTTCTAACCGAGGTCGA (SEQ ID NO:66). The 3' primer is the oligonucleotide TCACTTGAATCGCTGCATCTGCACCCCCAT (SEQ ID NO:67). Influenza virus from the America Type Tissue Collection (ATCC) is used as a source for the matrix coding region (Perdue *et al.* *Science* 279:393-396 (1998)), which is incorporated herein by reference (GenBank accession No. AF036358).

15 A DNA construct containing a pan DR epitope sequence (SEQ ID NO:38) fused to the amino-terminus of HBV-S antigen was generated (Figure 8). This construct is designated PADRE-HBV-s and was generated by annealing two overlapping oligonucleotides to add PADRE onto the amino terminus of hepatitis B surface antigen (Michel *et al.*, *Proc. Natl. Acad. Sci. USA* 81:7708-7712 (1984); Michel *et al.*, *Proc. Natl. Acad. Sci. USA* 92:5307-5311 (1995)), each of which is incorporated herein by reference. 20 One oligonucleotide was

GCTAGCGCCGCCACCATGGCCAAGTCGTGGCTGCCTGGACCCCTGAAGGGCTGC
25 CGCTC (SEQ ID NO:68). The second oligonucleotide was CTCGAGAGCGGCAGCCTTCAGGGTCCAGGCAGCCACGAACTTGGCCATGGTG GC GGCG (SEQ ID NO:69). When annealed, the oligos have NheI and XhoI cohesive ends. The oligos were heated to 100°C and slowly cooled to room temperature to anneal. A three part ligation joined PADRE with an XhoI-KpnI fragment containing HBV-s antigen into the NheI plus KpnI sites of the expression vector.

30 A DNA construct containing the signal sequence of Ig- α fused to the MHC class II epitope string shown in Figure 2 and the transmembrane and cytoplasmic domains of Ig- α was generated (Figure 9). The mouse Ig- α gene has been described previously (Kashiwamura *et al.*, *J. Immunol.* 145:337-343 (1990)), which is incorporated herein by reference (GenBank accession No. M31773). This construct, designated Ig-alphaTh, was constructed as depicted in Figure 18. The primer 1F used was the oligonucleotide

designated Ig alpha-1F, GCG GCT AGC GCC GCC ACC ATG CCA GGG GGT CTA (SEQ ID NO:70). The primer 1R used was the oligonucleotide designated Igalpha-1R, GCA CAG CCT GGC TGA TGG CCT GGC ATC CGG (SEQ ID NO:71). The primer 2F used was the oligonucleotide designated Igalpha-2F, CTG AAG GCT GCC GCT GGG 5 ATC ATC TTG CTG (SEQ ID NO:72). The primer 2R used was the oligonucleotide designated Igalpha-2R, GCG GGT ACC TCA TGG CTT TTC CAG CTG (SEQ ID NO:73).

A DNA construct containing the signal sequence of Ig- β fused to the MHC class II string shown in Figure 2 and the transmembrane and cytoplasmic domains of Ig β 10 was generated (Figure 10). The Ig- β sequence is the B29 gene of mouse and has been described previously (Hermanson *et al.*, *Proc. Natl. Acad. Sci. USA* 85:6890-6894 (1988)), which is incorporated herein by reference (GenBank accession No. J03857). This construct, designated Ig-betaTh, was constructed as depicted in Figure 18. The primer 1F used was the oligonucleotide designated B29-1F (33mer) GCG GCT AGC 15 GCC GCC ACC ATG GCC ACA CTG GTG (SEQ ID NO:74). The primer 1R used was the oligonucleotide designated B29-1R (30mer) CAC AGC CTG GCT GAT CGG CTC ACC TGA GAA (SEQ ID NO:75). The primer 2F used was the oligonucleotide designated B292F (30mer) CTG AAG GCT GCC GCT ATT ATC TTG ATC CAG (SEQ ID NO: 76). The primer 2R used was the oligonucleotide designated B29-2R (27mer), 20 GCC GGT ACC TCA TTC CTG GCC TGG ATG (SEQ ID NO:77).

A DNA construct containing the signal sequence of the kappa immunoglobulin signal sequence fused to the MHC class II epitope string shown in Figure 2 was constructed (Figure 11). This construct is designated SigTh and was generated by using the kappaLAMP-Th construct (shown in Figure 4) and amplifying 25 with the primer pair KappaSig-F (SEQ ID NO:54) plus Help-epR (SEQ ID NO:47) to create SigTh. SigTh contains the kappa immunoglobulin signal sequence fused to the T helper epitope string and terminated with a translational stop codon.

Constructs encoding human sequences corresponding to the above described constructs having mouse sequences are prepared by substituting human 30 sequences for the mouse sequences. Briefly, for the IiPADRE construct, corresponding to Figure 1, amino acid residues 1-80 from the human Ii gene HLA-DR sequence (Figure 12) (GenBank accession No. X00497 M14765) is substituted for the mouse Ii sequences, which is fused to PADRE, followed by human invariant chain HLA-DR amino acid residues 114-223. For the I80T construct, corresponding to Figure 2, amino acid residues

1-80 from the human sequence of Ii is followed by a MHC class II epitope string. For the IiThfull construct, corresponding to Figure 3, amino acid residues 1-80 from the human sequence of Ii, which is fused to a MHC class II epitope string, is followed by human invariant chain amino acid residues 114-223.

5 For the LAMP-Th construct, similar to Figure 4, the signal sequence encoded by amino acid residues 1-19 (nucleotides 11-67) of human LAMP-1 (Figure 13) (GenBank accession No. J04182), which is fused to the MHC class II epitope string, is followed by the transmembrane (nucleotides 1163-1213) and cytoplasmic tail (nucleotides 1214-1258) region encoded by amino acid residues 380-416 of human
10 LAMP-1.

For the HLA-DM-Th construct, corresponding to Figure 5, the signal sequence encoded by amino acid residues 1-17 (nucleotides 1-51) of human HLA-DMB (Figure 14) (GenBank accession No. U15085), which is fused to the MHC class II epitope string, is followed by the transmembrane (nucleotides 646-720) and cytoplasmic tail (nucleotides 721-792) region encoded by amino acid residues 216-263 of human HLA-
15 DMB.

For the HLA-DO-Th construct, corresponding to Figure 6, the signal sequence encoded by amino acid residues 1-21 (nucleotides 1-63) of human HLA-DO (Figure 15) (GenBank accession No. L29472 J02736 N00052), which is fused to the MHC class II epitope string, is followed by the transmembrane (nucleotides 685-735) and cytoplasmic tail (nucleotides 736-819) region encoded by amino acid residues 223-273 of
20 human HLA-DO.

For the Ig-alphaTh construct, corresponding to Figure 9, the signal sequence encoded by amino acid residues 1-29 (nucleotides 1-87) of human Ig- α MB-1 (Figure 16) (GenBank accession No. U05259), which is fused to the MHC class II epitope string, is followed by the transmembrane (nucleotides 424-498) and cytoplasmic tail (nucleotides 499-678) region encoded by amino acid residues 142-226 of human Ig- α MB-1.
25

For the Ig-betaTh construct, corresponding to Figure 10, the signal sequence encoded by amino acid residues 1-28 (nucleotides 17-100) of human Ig- β B29 (Figure 17) (GenBank accession No. M80461), which is fused to the MHC class II epitope string, is followed by the transmembrane (nucleotides 500-547) and cytoplasmic tail (nucleotides 548-703) region encoded by amino acid residues 156-229 of human Ig- β .
30

The SigTh construct shown in Figure 11 can be used in mouse and human. Alternatively, a signal sequence derived from an appropriate human gene containing a signal sequence can be substituted for the mouse kappa immunoglobulin sequence in the Sig Th construct.

5 The PADRE-Influenza matrix construct shown in Figure 7 and the PADRE-HBVs construct shown in Figure 8 can be used in mouse and human.

Some of the DNA constructs described above were cloned into the vector pEP2 (Figure 19; SEQ ID NO:35). The pEP2 vector was constructed to contain dual CMV promoters. The pEP2 vector used the backbone of pcDNA3.1(-)Myc-His A from 10 Invitrogen and pIRES1hyg from Clontech. Changes were made to both vectors before the CMV transcription unit from pIRES1hyg was moved into the modified pcDNA vector.

The pcDNA3.1(-)Myc-His A vector (<http://www.invitrogen.com>) was modified. Briefly, the PvuII fragment (nucleotides 1342-3508) was deleted. A BspHI fragment that contains the Ampicillin resistance gene (nucleotides 4404-5412) was cut out. The Ampicillin resistance gene was replaced with the kanamycin resistance gene 15 from pUC4K (GenBank Accession #X06404). pUC4K was amplified with the primer set: TCTGATGTTACATTGCACAAG (SEQ ID NO:78) (nucleotides 1621-1601) and GCGCACTCATGATGCTCTGCCAGTGTACAACC (SEQ ID NO:79) (nucleotides 682-702 plus the addition of a BspHI restriction site on the 5' end). The PCR product 20 was digested with BspHI and ligated into the vector digested with BspHI. The region between the PmeI site at nucleotide 905 and the EcoRV site at nucleotide 947 was deleted. The vector was then digested with PmeI (cuts at nucleotide 1076) and ApaI (cuts at nucleotide 1004), Klenow filled in at the cohesive ends and ligated. The KpnI site at 25 nucleotide 994 was deleted by digesting with KpnI and filling in the ends with Klenow DNA polymerase, and ligating. The intron A sequence from CMV (GenBank accession M21295, nucleotides 635-1461) was added by amplifying CMV DNA with the primer set: GCGTAGAGTAAGTACCGCCTATAGACTC (SEQ ID NO:80) (nucleotides 635-655 plus an XbaI site on the 5' end) and CCGGCTAGCCTGCAGAAAAGACCCATGGAA (SEQ ID NO:81) (nucleotides 1461-1441 plus an NheI site on the 3' end). The PCR 30 product was digested with XbaI and NheI and ligated into the NheI site of the vector (nucleotide 895 of the original pcDNA vector) so that the NheI site was on the 3' end of the intron.

To modify the pIRES1hyg vector (GenBank Accession U89672, Clontech), the KpnI site (nucleotide 911) was deleted by cutting and filling in with

Klenow. The plasmid was cut with NotI (nucleotide 1254) and XbaI (nucleotide 3196) and a polylinker oligo was inserted into the site. The polylinker was formed by annealing the following two oligos:

GGCCGCAAGGAAAAAATCTAGAGTCGCCATAGACTAATGCCGGTACCG (SEQ ID NO:82) and

CTAGCGGTACCGGCATTAGTCTATGGCCCGACTCTAGATTTTCTTGC (SEQ ID NO:83). The resulting plasmid was cut with HincII and the fragment between HincII sites 234 and 3538 was isolated and ligated into the modified pcDNA vector. This fragment contains a CMV promoter, intron, polylinker, and polyadenylation signal.

The pIREShyg piece and the pcDNA piece were combined to form pEP2. The modified pcDNA3.1(-)Myc-His A vector was partially digested with PvuII to isolate a linear fragment with the cut downstream of the pcDNA polyadenylation signal (the other PvuII site is the CMV intron). The HincII fragment from the modified pIRES1hyg vector was ligated into the PvuII cut vector. The polyadenylation signal from the pcDNA derived transcription unit was deleted by digesting with EcoRI (pcDNA nucleotide 955) and Xhol (pIRES1hyg nucleotide 3472) and replaced with a synthetic polyadenylation sequence. The synthetic polyadenylation signal was described in Levitt *et al.*, *Genes and Development* 3:1019-1025 (1989)).

Two oligos were annealed to produce a fragment that contained a polylinker and polyadenylation signal with EcoRI and XhoI cohesive ends. The oligos were:

AATTGGATATCCAAGCTTGATGAATAAAAGATCAGAGCTCTAGTGATCTGTGT
GTTGGTTTTTGTGTGC (SEQ ID NO:84) and

TCGAGCACACAAAAAACCAACACACAGATCACTAGAGCTCTGATCTTTATT
CATCAAGCTGGATATCCG (SEQ ID NO:85).

The resulting vector is named pEP2 and contains two separate transcription units. Both transcription units use the same CMV promoter but each contains different intron, polylinker, and polyadenylation sequences.

The pEP2 vector contains two transcription units. The first transcription unit contains the CMV promoter initially from pcDNA (nucleotides 210-862 in Figure 19), CMV intron A sequence (nucleotides 900-1728 in Figure 19), polylinker cloning site (nucleotides 1740-1760 in Figure 19) and synthetic polyadenylation signal (nucleotides 1764-1769 in Figure 19). The second transcription unit, which was initially derived from pIRES1hyg, contains the CMV promoter (nucleotides 3165-2493 in Figure 19), intron

sequence (nucleotides 2464-2173 in Figure 19), polylinker clone site (nucleotides 2126-2095 in Figure 19) and bovine growth hormone polyadenylation signal (nucleotides 1979-1974 in Figure 19). The kanamycin resistance gene is encoded in nucleotides 4965-4061 (Figure 19).

5 The DNA constructs described above were digested with NheI and KpnI and cloned into the XbaI and KpnI sites of pEP2 (the second transcription unit).

Additional vectors were also constructed. To test for the effect of co-expression of MHC class I epitopes with MHC class II epitopes, an insert was generated, designated AOS, that contains nine MHC class I epitopes. The AOS insert was initially 10 constructed in the vector pMIN.0 (Figure 20; SEQ ID NO:36). Briefly, the AOS insert contains nine MHC class I epitopes, six restricted by HLA-A2 and three restricted by HLA-A11, and the universal MHC class II epitope PADRE. The vector pMIN.0 contains epitopes from HBV, HIV and a mouse ovalbumin epitope. The MHC class I epitopes appear in pMIN.0 in the following order:

15 consensus mouse Ig Kappa signal sequence (pMIN.0 amino acid residues 1-20, nucleotides 16-81) MQVQIQSLFLLLLWVPGSSRG (SEQ ID NO:86) encoded by nucleotides ATG CAG GTG CAG ATC CAG AGC CTG TTT CTG CTC CTC CTG TGG GTG CCC GGG TCC AGA GGA (SEQ ID NO:87);

 HBV pol 149-159 (A11 restricted)

20 (pMIN.0 amino acid residues 21-31, nucleotides 82-114)
 HTLWKAGILYK (SEQ ID NO:88) encoded by nucleotides CAC ACC CTG TGG AAG GCC GGA ATC CTG TAT AAG (SEQ ID NO:89);

 PADRE-universal MHC class II epitope (pMIN.0 amino acid residues 32-45, nucleotides 115-153) AKFVAAWTLKAAA (SEQ ID NO:38) encoded by nucleotides 25 GCC AAG TTC GTG GCT GCC TGG ACC CTG AAG GCT GCC GCT (SEQ ID NO:90);

 HBV core 18-27 (A2 restricted) (pMIN.0 amino acid residues 46-55, nucleotides 154-183) FLPSDFFPSV (SEQ ID NO:91) encoded by nucleotides TTC CTG CCT AGC GAT TTC TTT CCT AGC GTG (SEQ ID NO:92);

30 HIV env 120-128 (A2 restricted) (pMIN.0 amino acid residues 56-64, nucleotides 184-210) KLTPLCVTL (SEQ ID NO:93) encoded by nucleotides AAG CTG ACC CCA CTG TGC GTG ACC CTG (SEQ ID NO:94);

HBV pol 551-559 (A2 restricted) (pMIN.0 amino acid residues 65-73, nucleotides 211-237) YMDDVVLGA (SEQ ID NO:95) encoded by nucleotides TAT ATG GAT GAC GTG GTG CTG GGA GCC (SEQ ID NO:96);

5 mouse ovalbumin 257-264 (K^b restricted) (pMIN.0 amino acid residues 74-81, nucleotides 238-261) SIINFEKL (SEQ ID NO:97) encoded by nucleotides AGC ATC ATC AAC TTC GAG AAG CTG (SEQ ID NO:98);

HBV pol 455-463 (A2 restricted) (pMIN.0 amino acid residues 82-90, nucleotides 262-288) GLSRYVARL (SEQ ID NO:99) encoded by nucleotides GGA CTG TCC AGA TAC GTG GCT AGG CTG (SEQ ID NO:100);

10 HIV pol 476-84 (A2 restricted) (pMIN.0 amino acid residues 91-99, nucleotides 289-315) ILKEPVHGV (SEQ ID NO:101) encoded by nucleotides ATC CTG AAG GAG CCT GTG CAC GGC GTG (SEQ ID NO:102);

HBV core 141-151 (A11 restricted)
(pMIN.0 amino acid residues 100-110, nucleotides 316-348)

15 STLPEVVVR (SEQ ID NO:103) encoded by nucleotides TCC ACC CTG CCA GAG ACC ACC GTG GTG AGG AGA (SEQ ID NO:104);

HIV env 49-58 (A11 restricted) (pMIN.0 amino acid residues 111-120, nucleotides 349-378) TVYYGVPWK (SEQ ID NO:105) encoded by nucleotides ACC GTG TAC TAT GGA GTG CCT GTG TGG AAG (SEQ ID NO:106); and

20 HBV env 335-343 (A2 restricted) (pMIN.0 amino acid residues 121-129, nucleotides 378-405) WLSLLVPFV (SEQ ID NO:107) encoded by nucleotides TGG CTG AGC CTG CTG GTG CCC TTT GTG (SEQ ID NO:108).

The pMIN.0 vector contains a KpnI restriction site (pMIN.0 nucleotides 406-411) and a NheI restriction site (pMIN.0 nucleotides 1-6). The pMIN.0 vector 25 contains a consensus Kozak sequence (nucleotides 7-18) (GCCGCCACCATG; SEQ ID NO:109) and murine Kappa Ig-light chain signal sequence followed by a string of 10 MHC class I epitopes and one universal MHC class II epitope. The pMIN.0 sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector. The pMIN.0 vector was constructed with eight 30 oligonucleotides:

Min1 oligo

GAGGAGCAGAACAGGGCTCTGGATCTGCACCTGCATTCCATGGTGGCGGCGC
TAGCAAGCTTCTGCGC (SEQ ID NO:110);

Min2 oligo

CCTGTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATA (SEQ ID NO:111);

Min3 oligo

5 TCGCTAGGCAGGAAAGCGGCAGCCTCAGGGTCCAGGCAGCCACGAACCTGG
CCTTATACAGGATTCCGG (SEQ ID NO:112);

Min4 oligo

CTTCCTGCCTAGCGATTCTTCCTAGCGTAAGCTGACCCCCTGTGCGTGA
CCCTGTATATGGATGAC (SEQ ID NO:113);

10 Min5 oligo

CGTACCTGGACAGTCCCAGCTCTCGAAGTTGATGATGCTGGCT
CCCAGCACACGTCATCCATATACAG (SEQ ID NO:114);

Min6 oligo

GGACTGTCCAGATACTGGCTAGGCTGATCCTGAAGGAGCCTGTGCACGGCGT
15 GTCCACCCTGCCAGAGAC (SEQ ID NO:115);

Min7 oligo

GCTCAGCCACTTCCACACAGGCCTCCATAGTACACGGTCCTCCTCACACGG
TGGTCTCTGGCAGGGTG (SEQ ID NO:116);

Min8 oligo

20 GTGGAAGTGGCTGAGCCTGCTGGTGCCCTTGTGGGTACCTGATCTAGAGC
(SEQ ID NO:117).

Additional primers were flanking primer 5', GCG CAA GAA GCT TGC
TAG CG (SEQ ID NO:118) and flanking primer 3', GCT CTA GAT CAG GTA CCC
CAC (SEQ ID NO:119).

25 The original pMIN.0 minigene construction was carried out using eight
overlapping oligos averaging approximately 70 nucleotides in length, which were
synthesized and HPLC purified by Operon Technologies Inc. Each oligo overlapped its
neighbor by 15 nucleotides, and the final multi-epitope minigene was assembled by
extending the overlapping oligos in three sets of reactions using PCR (Ho *et al.*, *Gene*
30 77:51-59 (1989).

For the first PCR reaction, 5 µg of each of two oligos were annealed and
extended: 1+2, 3+4, 5+6, and 7+8 were combined in 100 µl reactions containing 0.25 mM
each dNTP and 2.5 units of Pfu polymerase in Pfu polymerase buffer containing 10 mM
KCl, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% TRITON

X-100 and 100 mg/ml BSA. A Perkin/Elmer 9600 PCR machine was used and the annealing temperature used was 5°C below the lowest calculated T_m of each primer pair. The full length dimer products were gel-purified, and two reactions containing the product of 1-2 and 3-4, and the product of 5-6 and 7-8 were mixed, annealed and 5 extended for 10 cycles. Half of the two reactions were then mixed, and 5 cycles of annealing and extension carried out before flanking primers were added to amplify the full length product for 25 additional cycles. The full length product was gel purified and cloned into pCR-blunt (Invitrogen) and individual clones were screened by sequencing. The Min insert was isolated as an NheI-KpnI fragment and cloned into the same sites of 10 pcDNA3.1(-)/Myc-His A (Invitrogen) for expression. The Min protein contains the Myc and His antibody epitope tags at its carboxyl-terminal end.

For all the PCR reactions described, a total of 30 cycles were performed using Pfu polymerase and the following conditions: 95°C for 15 seconds, annealing temperature for 30 seconds, 72°C for one minute. The annealing temperature used was 15 5°C below the lowest calculated T_m of each primer pair.

Three changes to pMIN.0 were made to produce pMIN.1 (Figure 21; SEQ ID NO:37, also referred to as pMIN-AOS). The mouse ova epitope was removed, the position 9 alanine anchor residue (#547) of HBV pol 551-560 was converted to a valine which increased the *in vitro* binding affinity 40-fold, and a translational stop codon was 20 introduced at the end of the multi-epitope coding sequence. The changes were made by amplifying two overlapping fragments and combining them to yield the full length product.

The first reaction used the 5' pcDNA vector primer T7 and the primer Min-ovaR (nucleotides 247-218) TGGACAGTCCCCTCCAGCACCACGTCA (SEQ ID 25 NO:120). The 3' half was amplified with the primers: Min-ovaF (nucleotides 228-257) GCTGGGAGTGGGACTGTCCAGGTACGTGGC (SEQ ID NO:121) and Min-StopR (nucleotides 390-361) GGTACCTCACACAAAGGGCACCAGCAGGC (SEQ ID NO:122)

The two fragments were gel purified, mixed, denatured, annealed, and 30 filled in with five cycles of PCR. The full length fragment was amplified with the flanking primers T7 and Min-Stop for 25 more cycles. The product was gel purified, digested with NheI and KpnI and cloned into pcDNA3.1 for sequencing and expression. The insert from pMin.1 was isolated as an NheI-KpnI fragment and cloned into pEP2 to make pEP2-AOS.

EXAMPLE II: Assay for T Helper Cell Activation

This example shows methods for assaying T helper cell activity. One method for assaying T helper cell activity uses spleen cells of an immunized organism.

5 Briefly, a spleen cell pellet is suspended with 2-3 ml of red blood cell lysis buffer containing 8.3 g/liter ammonium chloride in 0.001 M Tris-HCl, pH 7.5. The cells are incubated in lysis buffer for 3-5 min at room temperature with occasional vortexing. An excess volume of 50 ml of R10 medium is added to the cells, and the cells are pelleted. The cells are resuspended and pelleted one or two more times in R2 medium or R10

10 medium.

The cell pellet is suspended in R10 medium and counted. If the cell suspension is aggregated, the aggregates are removed by filtration or by allowing the aggregates to settle by gravity. The cell concentration is brought to 10^7 /ml, and 100 μ l of spleen cells are added to 96 well flat bottom plates.

15 Dilutions of the appropriate peptide, such as pan DR epitope (SEQ ID NO:145), are prepared in R10 medium at 100, 10, 1, 0.1 and 0.01 μ g/ml, and 100 μ l of peptide are added to duplicate or triplicate wells of spleen cells. The final peptide concentration is 50, 5, 0.5, 0.05 and 0.005 μ g/ml. Control wells receive 100 μ l R10 medium.

20 The plates are incubated for 3 days at 37°C. After 3 days, 20 μ l of 50 μ Ci/ml 3 H-thymidine is added per well. Cells are incubated for 18-24 hours and then harvested onto glass fiber filters. The incorporation of 3 H-thymidine into DNA of proliferating cells is measured in a beta counter.

A second assay for T helper cell activity uses peripheral blood
25 mononuclear cells (PBMC) that are stimulated *in vitro* as described in Alexander *et al.*, *supra* and Sette (WO 95/07,707), as adapted from Manca *et al.*, *J. Immunol.* 146:1964-1971 (1991), which is incorporated herein by reference. Briefly, PBMC are collected from healthy donors and purified over Ficoll-Plaque (Pharmacia Biotech; Piscataway, NJ). PBMC are plated in a 24 well tissue culture plate at 4×10^6 cells/ml. Peptides are added at a final concentration of 10 μ g/ml. Cultures are incubated at 37°C in 5% CO₂.

30 On day 4, recombinant interleukin-2 (IL-2) is added at a final concentration of 10 ng/ml. Cultures are fed every 3 days by aspirating 1 ml of medium and replacing with fresh medium containing IL-2. Two additional stimulations of the T cells with antigen are performed on approximately days 14 and 28. The T cells ($3 \times$

10^5 /well) are stimulated with peptide ($10 \mu\text{g}/\text{ml}$) using autologous PBMC cells (2×10^6 irradiated cells/well) (irradiated with 7500 rads) as antigen-presenting cells in a total of three wells of a 24 well tissue culture plate. In addition, on day 14 and 28, T cell proliferative responses are determined under the following conditions: 2×10^4 T 5 cells/well; 1×10^5 irradiated PBMC/well as antigen-presenting cells; peptide concentration varying between 0.01 and $10 \mu\text{g}/\text{ml}$ final concentration. The proliferation of the T cells is measured 3 days later by the addition of ^3H -thymidine ($1 \mu\text{Ci}/\text{well}$) 18 hr prior to harvesting the cells. Cells are harvested onto glass filters and ^3H -thymidine incorporation is measured in a beta plate counter. These results demonstrate methods for 10 assaying T helper cell activity by measuring ^3H -thymidine incorporation.

EXAMPLE III: Assay for Cytotoxic T Lymphocyte Response

This example shows a method for assaying cytotoxic T lymphocyte (CTL) activity. A CTL response is measured essentially as described previously (Vitiello *et al.*, 15 *Eur. J. Immunol.* 27:671-678 (1997), which is incorporated herein by reference). Briefly, after approximately 10-35 days following DNA immunization, splenocytes from an animal are isolated and co-cultured at 37°C with syngeneic, irradiated (3000 rad) peptide-coated LPS blasts (1×10^6 to 1.5×10^6 cells/ml) in 10 ml R10 in T25 flasks. LPS blasts are obtained by activating splenocytes (1×10^6 to 1.5×10^6 cells/ml) with $25 \mu\text{g}/\text{ml}$ 20 lipopolysaccharides (LPS) (Sigma cat. no. L-2387; St. Louis, MO) and $7 \mu\text{g}/\text{ml}$ dextran sulfate (Pharmacia Biotech) in 30 ml R10 medium in T75 flasks for 3 days at 37°C . The lymphoblasts are then resuspended at a concentration of 2.5×10^7 to $3.0 \times 10^7/\text{ml}$, 25 irradiated (3000 rad), and coated with the appropriate peptides ($100 \mu\text{g}/\text{ml}$) for 1 h at 37°C . Cells are washed once, resuspended in R10 medium at the desired concentration and added to the responder cell preparation. Cultures are assayed for cytolytic activity on day 7 in a ^{51}Cr -release assay.

For the ^{51}Cr -release assay, target cells are labeled for 90 min at 37°C with 150 μl sodium ^{51}Cr chromate (^{51}Cr) (New England Nuclear; Wilmington DE), washed three times and resuspended at the appropriate concentration in R10 medium. For the assay, 30 10^4 target cells are incubated in the presence of different concentrations of effector cells in a final volume of 200 μl in U-bottom 96 well plates in the presence or absence of $10 \mu\text{g}/\text{ml}$ peptide. Supernatants are removed after 6 h at 37°C , and the percent specific lysis is determined by the formula: percent specific lysis = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison

of responses from different experiments, the percent release data is transformed to lytic units 30 per 10^6 cells (LU30/ 10^6), with 1 LU30 defined as the number of effector cells required to induce 30% lysis of 10^4 target cells in a 6 h assay. LU values represent the LU30/ 10^6 obtained in the presence of peptide minus LU30/ 10^6 in the absence of peptide.

- 5 These results demonstrate methods for assaying CTL activity by measuring ^{51}Cr release from cells.

EXAMPLE IV: T Cell Proliferation in Mice Immunized with Expression Vectors

Encoding MHC Class II Epitopes and MHC Class II Targeting Sequences

10 This example demonstrates that expression vectors encoding MHC class II epitopes and MHC class II targeting sequences are effective at activating T cells.

The constructs used in the T cell proliferation assay are described in Example I and were cloned into the vector pEP2, a CMV driven expression vector. The peptides used for T cell *in vitro* stimulation are: Ova 323-339, ISQAVHAAHAEINEAGR
15 (SEQ ID NO:123); HBVcore128, TPPAYRPPNAPILF (SEQ ID NO:124); HBVenv182, FFLLTRILTIPQSLD (SEQ ID NO:125); and PADRE, AKFVAAWTLKAAA (SEQ ID NO:38).

T cell proliferation was assayed essentially as described in Example II. Briefly, 12 to 16 week old B6D2 F1 mice (2 mice per construct) were injected with 100
20 μg of the indicated expression vector ($50 \mu\text{g}$ per leg) in the anterior tibialis muscle. After eleven days, spleens were collected from the mice and separated into a single cell suspension by Dounce homogenization. The splenocytes were counted and one million splenocytes were plated per well in a 96-well plate. Each sample was done in triplicate.
25 Ten $\mu\text{g}/\text{ml}$ of the corresponding peptide encoded by the respective expression vectors was added to each well. One well contained splenocytes without peptide added for a negative control. Cells were cultured at 37°C , 5% CO_2 for three days.

After three days, one μCi of ^3H -thymidine was added to each well. After 18 hours at 37°C , the cells were harvested onto glass filters and ^3H incorporation was measured on an LKB β plate counter. The results of the T cell proliferation assay are
30 shown in Table 9. Antigen-specific T cell proliferation is presented as the stimulation index (SI); this is defined as the ratio of the average ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

The immunogen "PADRE + IFA" is a positive control where the PADRE peptide in incomplete Freund's adjuvant was injected into the mice and compared to the

response seen by injecting the MHC class II epitope constructs containing a PADRE sequence. As shown in Table 9, most of the expression vectors tested were effective at activating T cell proliferation in response to the addition of PADRE peptide. The activity of several of the expression vectors was comparable to that seen with immunization with 5 the PADRE peptide in incomplete Freund's adjuvant. The expression vectors containing both MHC class I and MHC class II epitopes, pEP2-AOS and pcDNA-AOS, were also effective at activating T cell proliferation in response to the addition of PADRE peptide.

These results show that expression vectors encoding MHC class II epitopes fused to a MHC class II targeting sequence is effective at activating T cell 10 proliferation and are useful for stimulating an immune response.

EXAMPLE V: *In vivo* assay Using Transgenic Mice

A. Materials and methods

Peptides were synthesized according to standard F-moc solid phase 15 synthesis methods which have been previously described (Ruppert *et al.*, *Cell* 74:929 (1993); Sette *et al.*, *Mol. Immunol.* 31:813 (1994)). Peptide purity was determined by analytical reverse-phase HPLC and purity was routinely >95%. Synthesis and purification of the Theradigm-HBV lipopeptide vaccine is described in (Vitiello *et al.*, *J. Clin. Invest.* 95:341 (1995)).

20

Mice

HLA-A2.1 transgenic mice used in this study were the F1 generation derived by crossing transgenic mice expressing a chimeric gene consisting of the $\alpha 1$, $\alpha 2$ domains of HLA-A2.1 and $\alpha 3$ domain of H-2K^b with SJL/J mice (Jackson Laboratory, 25 Bar Harbor, ME). This strain will be referred to hereafter as HLA-A2.1/K^b-H-2^{bxs}. The parental HLA-A2.1/K^b transgenic strain was generated on a C57BL/6 background using the transgene and methods described in (Vitiello *et al.*, *J. Exp. Med.* 173:1007 (1991)). HLA-A11/K^b transgenic mice used in the current study were identical to those described in (Alexander *et al.*, *J. Immunol.* 159:4753 (1997)).

30

Cell lines, MHC purification, and peptide binding assay

Target cells for peptide-specific cytotoxicity assays were Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (Vitiello *et al.*, *J. Exp. Med.* 173:1007

(1991)) and .221 tumor cells transfected with HLA-A11/K^b (Alexander *et al.*, *J. Immunol.* 159:4753 (1997)).

To measure presentation of endogenously processed epitopes, Jurkat-A2.1/K^b cells were transfected with the pMin.1 or pMin.2-GFP minigenes then tested in a cytotoxicity assay against epitope-specific CTL lines. For transfection, Jurkat-A2.1/K^b cells were resuspended at 10⁷ cells/ml and 30 µg of DNA was added to 600 µl of cell suspension. After electroporating cells in a 0.4 cm cuvette at 0.25 kV, 960 µFd, cells were incubated on ice for 10 min then cultured for 2 d in RPMI culture medium. Cells were then cultured in medium containing 200 U/ml hygromycin B (Calbiochem, San Diego CA) to select for stable transfectants. FACS was used to enrich the fraction of green fluorescent protein (GFP)-expressing cells from 15% to 60% (data not shown).

Methods for measuring the quantitative binding of peptides to purified HLA-A2.1 and -A11 molecules is described in Ruppert *et al.*, *Cell* 74:929 (1993); Sette *et al.*, *Mol. Immunol.* 31:813 (1994); Alexander *et al.*, *J. Immunol.* 159:4753 (1997).

All tumor cell lines and splenic CTLs from primed mice were grown in culture medium (CM) that consisted of RPMI 1640 medium with Hepes (Life Technologies, Grand Island, NY) supplemented with 10% FBS, 4 mM L-glutamine, 5 X 10⁻⁵ M 2-ME, 0.5 mM sodium pyruvate, 100 µg/ml streptomycin, and 100 U/ml penicillin.

20

Construction of minigene multi-epitope DNA plasmids

pMIN.0 and pMIN.1 (i.e., pMIN-AOS) were constructed as described above and in USSN 60/085,751.

25

pMin.1-No PADRE and pMin.1-Anchor. pMin.1 was amplified using two overlapping fragments which was then combined to yield the full length product. The first reaction used the 5' pcDNA vector primer T7 and either primer ATCGCTAGGCAGGAACCTTATACAGGATTCC (SEQ ID NO:126) for pMin.1-No PADRE or TGGACAGTCCGGCTCCCAGCACACGT (SEQ ID NO:127) for pMin.1-Anchor. The 3' half was amplified with the primers TTCCTGCCTAGCGATTTC (SEQ ID NO:128) (No PADRE) or GCTGGGAGCCGGACTGTCCAGGTACGT (SEQ ID NO:129) (Anchor) and Min-StopR. The two fragments generated from amplifying the 5' and 3' ends were gel purified, mixed, denatured, annealed, and filled in with five cycles

of PCR. The full length fragment was further amplified with the flanking primers T7 and Min-StopR for 25 more cycles.

pMin.1-No Sig. The Ig signal sequence was deleted from pMin.1 by PCR
5 amplification with primer GCTAGCGCCGCCACCATGCACACCCTGTGGAAGGC
CGGAATC (SEQ ID NO:130) and pcDNA rev (Invitrogen) primers. The product was
cloned into pCR-blunt and sequenced.

pMin.1-Switch. Three overlapping fragments were amplified from
10 pMin.1, combined, and extended. The 5' fragment was amplified with the vector primer
T7 and primer GGGCACCAAGCAGGCTCAGCCACACTCCCAGCACCACGTC (SEQ
ID NO:131). The second overlapping fragment was amplified with primers
AGCCTGCTGGTGCCCTTGATCCTGAAGGAGCCTGTGC (SEQ ID NO:132)
and AGCCACGTACCTGGACAGTCCCTCCACACAGGCACCTCCAT (SEQ ID
15 NO:133). Primer TGTCCAGGTACGTGGCTAGGCTGTGAGGTACC (SEQ ID
NO:134) and the vector primer pcDNA rev (Invitrogen) were used to amplify the third
(3') fragment. Fragments 1, 2, and 3 were amplified and gel purified. Fragments 2 and 3
were mixed, annealed, amplified, and gel purified. Fragment 1 was combined with the
product of 2 and 3, and extended, gel purified and cloned into pcDNA3.1 for expression.

20

pMin.2-GFP. The signal sequence was deleted from pMin.0 by PCR
amplification with Min.0-No Sig-5' plus pcDNA rev (Invitrogen) primers
GCTAGCGCCGCCACCATGCACACCCTGTGGAAGGCCGGAATC (SEQ ID
NO:135). The product was cloned into pCR-blunt and sequenced. The insert containing
25 the open reading frame of the signal sequence-deleted multi-epitope construct was cut out
with *Nhe*I plus *Hind*III and ligated into the same sites of pEGFPN1 (Clontech). This
construct fuses the coding region of the signal-deleted pMin.0 construct to the N-terminus
of green fluorescent protein (GFP).

30

Immunization of mice

For DNA immunization, mice were pretreated by injecting 50 µl of 10 µM
cardiotoxin (Sigma Chem. Co., #C9759) bilaterally into the tibialis anterior muscle. Four
or five days later, 100 µg of DNA diluted in PBS were injected in the same muscle.

Theradigm-HBV lipopeptide (10 mg/ml in DMSO) that was stored at -20°C, was thawed for 10 min at 45°C before being diluted 1:10 (v/v) with room temperature PBS. Immediately upon addition of PBS, the lipopeptide suspension was vortexed vigorously and 100 µl was injected s.c. at the tail base (100 µg/mouse).

5 Immunogenicity of individual CTL epitopes was tested by mixing each CTL epitope (50 µg/mouse) with the HBV core 128-140 peptide (TPPA YRPPNAPIL (SEQ ID NO:124), 140 µg/mouse) which served to induce I-A^b-restricted Th cells. The peptide cocktail was then emulsified in incomplete Freund's adjuvant (Sigma Chem. Co.) and 100 µl of peptide emulsion was injected s.c. at the tail base.

10

In vitro CTL cultures and cytotoxicity assays

Eleven to 14 days after immunization, animals were sacrificed and a single cell suspension of splenocytes prepared. Splenocytes from cDNA-primed animals were stimulated *in vitro* with each of the peptide epitopes represented in the minigene. 15 Splenocytes (2.5-3.0 X 10⁷/flask) were cultured in upright 25 cm² flasks in the presence of 10 µg/ml peptide and 10⁷ irradiated spleen cells that had been activated for 3 days with LPS (25 µg/ml) and dextran sulfate (7 µg/ml). Triplicate cultures were stimulated with each epitope. Five days later, cultures were fed with fresh CM. After 10 d of *in vitro* culture, 2-4 X 10⁶ CTLs from each flask were restimulated with 10⁷ LPS/dextran sulfate- 20 activated splenocytes treated with 100 µg/ml peptide for 60-75 min at 37°C, then irradiated 3500 rads. CTLs were restimulated in 6-well plates in 8 ml of cytokine-free CM. Eighteen hr later, cultures received cytokines contained in con A-activated splenocyte supernatant (10-15% final concentration, v/v) and were fed or expanded on the third day with CM containing 10-15% cytokine supernate. Five days after restimulation, 25 CTL activity of each culture was measured by incubating varying numbers of CTLs with 10⁴ ⁵¹Cr-labelled target cells in the presence or absence of peptide. To decrease nonspecific cytotoxicity from NK cells, YAC-1 cells (ATCC) were also added at a YAC- 1:⁵¹Cr-labeled target cell ratio of 20:1. CTL activity against the HBV Pol 551 epitope was measured by stimulating DNA-primed splenocytes *in vitro* with the native A-containing peptide and testing for cytotoxic activity against the same peptide.

To more readily compare responses, the standard E:T ratio vs % cytotoxicity data curves were converted into LU per 10⁶ effector cells with one LU defined as the lytic activity required to achieve 30% lysis of target cells at a 100:1 E:T

ratio. Specific CTL activity (Δ LU) was calculated by subtracting the LU value obtained in the absence of peptide from the LU value obtained with peptide. A given culture was scored positive for CTL induction if all of the following criteria were met: 1) Δ LU > 2; 2) $\text{LU(+ peptide)} / \text{LU(- peptide)} > 3$; and 3) a > 10% difference in % cytotoxicity tested with and without peptide at the two highest E:T ratios (starting E:T ratios were routinely between 25-50:1).

5 CTL lines were generated from pMin.1-primed splenocytes through repeated weekly stimulations of CTLs with peptide-treated LPS/DxS-activated splenocytes using the 6-well culture conditions described above with the exception that 10 CTLs were expanded in cytokine-containing CM as necessary during the seven day stimulation period.

Cytokine assay

To measure IFN- γ production in response to minigene-transfected target 15 cells, 4×10^4 CTLs were cultured with an equivalent number of minigene-transfected Jurkat-A2.1/K^b cells in 96-well flat bottom plates. After overnight incubation at 37°C, culture supernatant from each well was collected and assayed for IFN- γ concentration using a sandwich ELISA. Immulon II microtiter wells (Dynatech, Boston, MA) were coated overnight at 4°C with 0.2 μ g of anti-mouse IFN- γ capture Ab, R4-6A2 20 (Pharmingen). After washing wells with PBS/0.1% Tween-20 and blocking with 1% BSA, Ab-coated wells were incubated with culture supernate samples for 2 hr at room temperature. A secondary anti-IFN- γ Ab, XMG1.2 (Pharmingen), was added to wells and allowed to incubate for 2 hr at room temperature. Wells were then developed by 25 incubations with Avidin-DH and finally with biotinylated horseradish peroxidase H (Vectastain ABC kit, Vector Labs, Burlingame, CA) and TMB peroxidase substrate (Kirkegaard and Perry Labs, Gaithersberg, MD). The amount of cytokine present in each sample was calculated using a rIFN- γ standard (Pharmingen).

b. Results

30 Selection of epitopes and minigene construct design

In the first series of experiments, the issue was whether a balanced multispecific CTL response could be induced by simple minigene cDNA constructs that encode several dominant HLA class I-restricted epitopes. Accordingly, nine CTL

epitopes were chosen on the basis of their relevance in CTL immunity during HBV and HIV infection in humans, their sequence conservancy among viral subtypes, and their class I MHC binding affinity (Table 10). Of these nine epitopes, six are restricted by HLA-A2.1 and three showed HLA-A11-restriction. One epitope, HBV Pol 551, was
5 studied in two alternative forms: either the wild type sequence or an analog (HBV Pol 551-V) engineered for higher binding affinity.

As referenced in Table 10, several independent laboratories have reported that these epitopes are part of the dominant CTL response during HBV or HIV infection. All of the epitopes considered showed greater than 75% conservancy in primary amino acid sequence among the different HBV subtypes and HIV clades. The MHC binding affinity of the peptides was also considered in selection of the epitopes. These experiments addressed the feasibility of immunizing with epitopes possessing a wide range of affinities and, as shown in Table 10, the six HBV and three HIV HLA-restricted epitopes covered a spectrum of MHC binding affinities spanning over two orders of magnitude, with IC₅₀% concentrations ranging from 3 nM to 200 nM.
10
15

The immunogenicity of the six A2.1- and three A11-restricted CTL epitopes in transgenic mice was verified by co-immunization with a helper T cell peptide in an IFA formulation. All of the epitopes induced significant CTL responses in the 5 to 73 ΔLU range (Table 10). As mentioned above, to improve the MHC binding and
20 immunogenicity of HBV Pol 551, the C-terminal A residue of this epitope was substituted with V resulting in a dramatic 40-fold increase in binding affinity to HLA-A2.1 (Table 10). While the parental sequence was weakly or nonimmunogenic in HLA transgenic mice, the HBV Pol 551-V analog induced significant levels of CTL activity when administered in IFA (Table 10). On the basis of these results, the V analog of the HBV
25 Pol 551 epitope was selected for the initial minigene construct. In all of the experiments reported herein, CTL responses were measured with target cells coated with the native HBV Pol 551 epitope, irrespective of whether the V analog or native epitope was utilized for immunization.

Finally, since previous studies indicated that induction of T cell help significantly improved the magnitude and duration of CTL responses (*Vitiello et al., J. Clin. Invest.* 95:341 (1995); *Livingston et al., J. Immunol.* 159:1383 (1997)), the universal Th cell epitope PADRE was also incorporated into the minigene. PADRE has been shown previously to have high MHC binding affinity to a wide range of mouse and
30

human MHC class II haplotypes (Alexander *et al.*, *Immunity* 1:751 (1994)). In particular, it has been previously shown that PADRE is highly immunogenic in H-2^b mice that are used in the current study (Alexander *et al.*, *Immunity* 1:751 (1994)).

5 pMin.1, the prototype cDNA minigene construct encoding nine CTL epitopes and PADRE, was synthesized and subcloned into the pcDNA3.1 vector. The position of each of the nine epitopes in the minigene was optimized to avoid junctional mouse H-2^b and HLA-A2.1 class I MHC epitopes. The mouse Ig κ signal sequence was also included at the 5' end of the construct to facilitate processing of the CTL epitopes in the endoplasmic reticulum (ER) as reported by others (Anderson *et al.*, *J. Exp. Med.* 10 174:489 (1991)). To avoid further conformational structure in the translated polypeptide 10 gene product that may affect processing of the CTL epitopes, an ATG stop codon was introduced at the 3' end of the minigene construct upstream of the coding region for c-myc and poly-his epitopes in the pcDNA3.1 vector.

15

Immunogenicity of pMin.1 in transgenic mice

To assess the capacity of the pMin.1 minigene construct to induce CTLs *in vivo*, HLA-A2.1/K^b-H-2^{bxs} transgenic mice were immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA 20 immunization, a control group of animals was also immunized with Theradigm-HBV, a palmitolyated lipopeptide consisting of the HBV Core 18 CTL epitope linked to the tetanus toxin 830-843 Th cell epitope.

Splenocytes from immunized animals were stimulated twice with each of the peptide epitopes encoded in the minigene, then assayed for peptide-specific cytotoxic activity in a ⁵¹Cr release assay. A representative panel of CTL responses of pMin.1- 25 primed splenocytes, shown in Figure 22, clearly indicates that significant levels of CTL induction were generated by minigene immunization. The majority of the cultures stimulated with the different epitopes exceeded 50% specific lysis of target cells at an E:T ratio of 1:1. The results of four independent experiments, compiled in Table 11, indicate that the pMin.1 construct is indeed highly immunogenic in HLA-A2.1/K^b-H-2^{bxs} 30 transgenic mice, inducing a broad CTL response directed against each of its six A2.1-restricted epitopes.

To more conveniently compare levels of CTL induction among the different epitopes, the % cytotoxicity values for each splenocyte culture was converted to

ΔLU and the mean ΔLU of CTL activity in positive cultures for each epitope was determined (see Example V, materials and methods, for positive criteria). The data, expressed in this manner in Table 11, confirms the breadth of CTL induction elicited by pMin.1 immunization since extremely high CTL responses, ranging between 50 to 700
5 ΔLU, were observed against the six A2.1-restricted epitopes. More significantly, the responses of several hundred ΔLU observed for five of the six epitopes approached or exceeded that of the Theradigm-HBV lipopeptide, a vaccine formulation known for its high CTL-inducing potency (Vitiello *et al.*, *J. Clin. Invest.* 95:341 (1995); Livingston *et al.*, *J. Immunol.* 159:1383 (1997)). The HBV Env 335 epitope was the only epitope
10 showing a lower mean ΔLU response compared to lipopeptide (Table 11, 44 vs 349 ΔLU).

Processing of minigene epitopes by transfected cells

The decreased CTL response observed against HBV Env 335 was somewhat unexpected since this epitope had good A2.1 binding affinity (IC50%, 5 nM) and was also immunogenic when administered in IFA. The lower response may be due, at least in part, to the inefficient processing of this epitope from the minigene polypeptide by antigen presenting cells following *in vivo* cDNA immunization. To address this possibility, Jurkat-A2.1-K^b tumor cells were transfected with pMin.1 cDNA and the presentation of the HBV Env 335 epitope by transfected cells was compared to more immunogenic A2.1-restricted epitopes using specific CTL lines. Epitope presentation was also studied using tumor cells transfected with a control cDNA construct, pMin.2-GFP, that encoded a similar multi-epitope minigene fused with GFP which allows detection of minigene expression in transfected cells by FACS.
25

Epitope presentation of the transfected Jurkat cells was analyzed using specific CTL lines, with cytotoxicity or IFN-γ production serving as a read-out. It was found that the levels of CTL response correlated directly with the *in vivo* immunogenicity of the epitopes. Highly immunogenic epitopes *in vivo*, such as HBV Core 18, HIV Pol 476, and HBV Pol 455, were efficiently presented to CTL lines by pMin.1- or pMin.2-GFP-transfected cells as measured by IFN-γ production (Figure 23A, >100 pg/ml for each epitope) or cytotoxic activity (Figure 23C, >30% specific lysis). In contrast to these high levels of *in vitro* activity, the stimulation of the HBV Env 335-specific CTL line against both populations of transfected cells resulted in less than 12 pg/ml IFN-γ and 3% specific
30

ysis. Although the HBV Env 335-specific CTL line did not recognize the naturally processed epitope efficiently, this line did show an equivalent response to peptide-loaded target cells, as compared to CTL lines specific for the other epitopes (Figure 23B, D). Collectively, these results suggest that a processing and/or presentation defect associated 5 with the HBV Env 335 epitope that may contribute to its diminished immunogenicity *in vivo*.

Effect of the helper T cell epitope PADRE on minigene immunogenicity

Having obtained a broad and balanced CTL response in transgenic mice 10 immunized with a minigene cDNA encoding multiple HLA-A2.1-restricted epitopes, next possible variables were examined that could influence the immunogenicity of the prototype construct. This type of analysis could lead to rational and rapid optimization of future constructs. More specifically, a cDNA construct based on the pMin.1 prototype was synthesized in which the PADRE epitope was deleted to examine the contribution of 15 T cell help in minigene immunogenicity (Figure 24A).

The results of the immunogenicity analysis indicated that deletion of the PADRE Th cell epitope resulted in significant decreases in the frequency of specific CTL precursors against four of the minigene epitopes (HBV Core 18, HIV Env 120, HBV Pol 455, and HBV Env 335) as indicated by the 17 to 50% CTL-positive cultures observed 20 against these epitopes compared to the 90-100% frequency in animals immunized with the prototype pMin.1 construct (Figure 25). Moreover, for two of the epitopes, HBV Core 18 and HIV Env 120, the magnitude of response in positive cultures induced by pMin.1-No PADRE was 20- to 30-fold less than that of the pMin.1 construct (Figure 25A).

25

Effect of modulation of MHC binding affinity on epitope immunogenicity

Next a construct was synthesized in which the V anchor residue in HBV Pol 551 was replaced with alanine, the native residue, to address the effect of decreasing MHC binding on epitope immunogenicity (Figure 24B).

30

Unlike deletion of the Th cell epitope, decreasing the MHC binding capacity of the HBV Pol 551 epitope by 40-fold through modification of the anchor residue did not appear to affect epitope immunogenicity (Figure 25B). The CTL response against the HBV Pol 551 epitope, as well as to the other epitopes, measured either by LU or frequency of CTL-positive cultures, was very similar between the constructs

containing the native A or improved V residue at the MHC binding anchor site. This finding reinforces the notion that minimal epitope minigenes can efficiently deliver epitopes of vastly different MHC binding affinities. Furthermore, this finding is particularly relevant to enhancing epitope immunogenicity via different delivery methods,
5 especially in light of the fact that the wild type HBV Pol 551 epitope was essentially nonimmunogenic when delivered in a less potent IFA emulsion.

Effect of the signal sequence on minigene construct immunogenicity

The signal sequence was deleted from the pMin.1 construct, thereby
10 preventing processing of the minigene polypeptide in the ER (Figure 24C). When the immunogenicity of the pMin.1-No Sig construct was examined, an overall decrease in response was found against four CTL epitopes. Two of these epitopes, HIV Env 120 and HBV Env 335, showed a decrease in frequency of CTL-positive cultures compared to pMin.1 while the remaining epitopes, HBV Pol 455 and HIV Pol 476, showed a 16-fold
15 (from 424 to 27 ΔLU) and 3-fold decrease (709 to 236 ΔLU) in magnitude of the mean CTL response, respectively (Figure 25C). These findings suggest that allowing ER-processing of some of the epitopes encoded in the pMin.1 prototype construct may improve immunogenicity, as compared with constructs that allow only cytoplasmic processing of the same panel of epitopes.
20

Effect of epitope rearrangement and creation of new junctional epitopes

In the final construct tested, the immunogenicity of the HBV Env 335 epitope was analyzed to determine whether it may be influenced by its position at the 3' terminus of the minigene construct (Figure 24D). Thus, the position of the Env epitope in
25 the cDNA construct was switched with a more immunogenic epitope, HBV Pol 455, located in the center of the minigene. It should be noted that this modification also created two potentially new epitopes. As shown in Figure 25D, the transposition of the two epitopes appeared to affect the immunogenicity of not only the transposed epitopes but also more globally of other epitopes. Switching epitopes resulted in obliteration of
30 CTL induction against HBV Env 335 (no positive cultures detected out of six). The CTL response induced by the terminal HBV Pol 455 epitope was also decreased but only slightly (424 vs 78 mean ΔLU). In addition to the switched epitopes, CTL induction against other epitopes in the pMin.1-Switch construct was also markedly reduced

compared to the prototype construct. For example, a CTL response was not observed against the HIV Env 120 epitope and it was significantly diminished against the HBV Core 18 (4 of 6 positive cultures, decrease in mean Δ LU from 306 to 52) and HBV Pol 476 (decrease in mean Δ LU from 709 to 20) epitopes (Figure 25D).

5 As previously mentioned, it should be noted that switching the two epitopes had created new junctional epitopes. Indeed, in the pMin.1-Switch construct, two new potential CTL epitopes were created from sequences of HBV Env 335-HIV Pol 476 (LLVPFVIL (SEQ ID NO:135), H-2K^b-restricted) and HBV Env 335-HBV Pol 551 (VLGVWLSLLV (SEQ ID NO:136), HLA-A2.1-restricted) epitopes. Although these 10 junctional epitopes have not been examined to determine whether or not they are indeed immunogenic, this may account for the low immunogenicity of the HBV Env 335 and HIV Pol 476 epitopes. These findings suggest that avoiding junctional epitopes may be important in designing multi-epitope minigenes as is the ability to confirm their immunogenicity *in vivo* in a biological assay system such as HLA transgenic mice.

15

Induction of CTLs against A11 epitopes encoded in pMin.1

To further examine the flexibility of the minigene vaccine approach for inducing a broad CTL response against not only multiple epitopes but also against epitopes restricted by different HLA alleles, HLA-A11/K^b transgenic mice were 20 immunized to determine whether the three A11 epitopes in the pMin.1 construct were immunogenic for CTLs, as was the case for the A2.1-restricted epitopes in the same construct. As summarized in Table 12, significant CTL induction was observed in a majority of cultures against all three of the HLA-A11-restricted epitopes and the level of CTL immunity induced for the three epitopes, in the range of 40 to 260 Δ LU, exceeded 25 that of peptides delivered in IFA (Table 10). Thus, nine CTL epitopes of varying HLA restrictions incorporated into a prototype minigene construct all demonstrated significant CTL induction *in vivo*, confirming that minigene DNA plasmids can serve as means of delivering multiple epitopes, of varying HLA restrictions and MHC binding affinities, to the immune system in an immunogenic fashion and that appropriate transgenic mouse 30 strains can be used to measure DNA construct immunogenicity *in vivo*.

CTLs were also induced against three A11 epitopes in A11/K^b transgenic mice. These responses suggest that minigene delivery of multiple CTL epitopes that confers broad population coverage may be possible in humans and that transgenic animals

of appropriate haplotypes may be a useful tools in optimizing the *in vivo* immunogenicity of minigene DNA. In addition, animals such as monkeys having conserved HLA molecules with cross reactivity to CTL and HTL epitopes recognized by human MHC molecules can be used to determine human immunogenicity of HTL and CTL epitopes
5 (Bertoni *et al.*, *J. Immunol.* 161:4447-4455 (1998)).

This study represents the first description of the use of HLA transgenic mice to quantitate the *in vivo* immunogenicity of DNA vaccines, by examining response to epitopes restricted by human HLA antigens. *In vivo* studies are required to address the variables crucial for vaccine development, that are not easily evaluated by *in vitro* assays,
10 such as route of administration, vaccine formulation, tissue biodistribution, and involvement of primary and secondary lymphoid organs. Because of its simplicity and flexibility, HLA transgenic mice represent an attractive alternative, at least for initial vaccine development studies, compared to more cumbersome and expensive studies in higher animal species, such as nonhuman primates. The *in vitro* presentation studies
15 described above further supports the use of HLA transgenic mice for screening DNA constructs containing human epitopes inasmuch as a direct correlation between *in vivo* immunogenicity and *in vitro* presentation was observed. Finally, strong CTL responses were observed against all six A 2.1 restricted viral epitopes and in three A11 restricted epitopes encoded in the prototype pMin.1 construct. For five of the A 2.1 restricted
20 epitopes, the magnitude of CTL response approximated that observed with the lipopeptide, Theradigm-HBV, that previously was shown to induce strong CTL responses in humans (Vitiello *et al.*, *J. Clin. Invest.* 95:341 (1995); Livingston *et al.*, *J. Immunol.* 159:1383 (1997)).

Table 1
HBV derived HTL epitopes

Peptide	Sequence	Source	SEQ ID NO:
I298.06	KQAFITFSPTYKAFLC	HBV POL 661	
F107.03	LQLSLTNLSSNLSSWL	HBV POL 412	
1280.06	AGFFLLTRILTRILTIPQS	HBV ENV 180	
1280.09	GTSFVYYVPSALNPAD	HBV POL 774	
CF-08	VSGFGVWIRKPAAYRPPNAPI	HBV NUC 120	
27.0280	GVWIK'IPPAAYRPPNA	HBV NUC 123	
1186.25	SIGUVWIK'IPPAAYRPPNA	HBV NUC 121	
27.0281	RHYLHTLWKAGILYK	HBV POL 145	
F107.04	PFLLAQFTSAICSVV	HBV POL 523	
1186.15	LVPFVQWFWVGLSPTV	HBV ENV 339	
1280.15	LHLYSHPDILGFRKI	HBV POL 501	
1298.04	KQCFRKLPVNRPIDW	HBV POL 615	
1298.07	AANWILRLRGTSFVYVP	HBV POL 764	
857.02	PIHHTALRQAIILCWGEMLMTLA	HBV CORE 50	
35.0100	LCQQVFADATPTGWWGL	HBV POL 683	
35.0096	ESRLVVDFSQFSRGN	HBV POL 387	
35.0093	VGPLTVNEKRLKLII	HBV POL 96	
1186.18	NLSWLSLDVSAAFYH	HBV POL 422	

Table 2
HBV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A2	924.07 1013.0102 777.03 927.15 1168.02 927.11	FIPSDIFPSV W1SL1LYPFV F1LTRHITI ALMPLYACI GLSRYYVARL FLISLGHL	HBV core 18-27 HBV adr-ENV (S Ag 33.5-34.3) HBV Env ayw 183 HBV ayw pol 642 HBV POL 455 HBV pol 562	
	1147.16 1083.01 1090.11 1090.10 1069.16 1069.20 1142.05 1069.15	HTLWKAGILYK STLPETIYVRR SAICSVVRK QATITPSPTYK NVSIIPWTIK LVVDFSQFSR KVGNIFTGLY TLWKAGILYK	HBV POL 149 HBV core 141 HBV pol 531 HBV pol 665 HBV pol 47 HBV pol 388 HBV adr POL 629 HBV pol 150	
	1145.04 988.05 1147.04	IPSSSWAF LPSSDFFPSSV TPARVITGGVF	HBV ENV 313 HBV core 19-27 HBV POL 354	
	1069.06 1147.13 1147.14 1132.01 1069.05 9227.42 9227.41 9227.46 1069.071 1142.07 9227.47 1069.13 1013.1402 1090.14	LLVPFVQWFW FLLAQFTSAI VLLDYQQGMLPV LVPPVQWFW L.I.AQFISAI NL.SWI.SI.DV L.I.SSNLSWL KL.IILYSHPI F.I.LAQFTSA GLJ.GWSPIQA HLYSHIPIL PL.PIFFCL VI.QAGFPL YMDDVVLGA	HBV env 338-347 HBV POL 513 HBV ENV 259 HBV ENV 339 HBV pol 504-512 HBV pol 411 HBV pol 992 HBV pol 489 HBV pol 503 HBV ENV 62 HBV ayw pol 1076 HBV env 377-385 HBV adr-ENV 177 HBV pol 538-546	
	26.0539 26.0535	RLVVDFSQFSR GVWRTRPPAYR	HBV pol 376 HBV X nuc fus 299	
A3				

Table 2 (Cont'd)
HBV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A3	26.0153 1.0993	SSAGPCALR KVFVLGGCR CALMFTSAR	HBV X 64 HBV adr "X" 1548 HBV X 69	
	26.0149	VSGFVVWIR	HBV x nuc fus 296	
	26.0023	TLPETTVVIRR	HBV x nuc fus 318	
	26.0545	SVVRRAFPH	HBV POL 524	
	20.0131	FVIGGCRIK	HBV adr "X" 1550	
	1.0219	FITSPTYK	HBV pol 656	
	26.0008	AFTESPTYK	HBV POL 655	
	20.0130	FPHCLAFSYM YPALMPLYA	HBV POL S30 HBV POL 640	
	1147.05	LPCVAIASSA	HBV X 58	
	1147.08	HPAAMPILL	HBV POL 429	
B7	1147.06	YPAIMPLYACI	HBV pol 640	
	1147.02	YPALMPLY	HBV POL 640	
	26.0570	FPHCLAFSY	HBV POL 541	
	19.0014	AYRPPNAPI	HBV NUC 131	
	1145.08	DLLDTASALY	HBV adr CORE 419	
	1090.02	EYLVSFGVWI	HBV NUC 117	
	1.0519	FAAPFTQCGY	HBV POL 631	
	13.0129	GYPALMPLY	HBV ALL 1224	
	20.0234	ITLWKAGILY	HBV pol 149	
	2.0060	ILLCCLFL	HBV env 249-258	
Other	1069.04	KVGNFTGLY	HBV adr POL 629	
	1069.08	KYTSPFWILL	HBV POL 745	
	1.0166	I.DTASALY	HBV core 59	
	1069.23	I.SLDVSAAFY	HBV ALL 1000	
	1069.01	LYSHPHILGF	HBV POL 492	
	2.0239	MMWYWGSLY	HBV 360	
	2.0181	MSTTDLEAY	HBV adr 1521	
	1039.01	PLDKGKPKYY	HBV pol 124	
	2.0126	PTGGRTSLY	HBV pol 808	
	1069.03	PWTIKVGINF	HBV POL 51	
	1090.09	RWMCLRRFI	HBV ENV 236	
	20.0138	RWMCLRRFII	HBV ENV 236	
	20.0135	SFCGSPYSW	HBV POL 167	
	20.0269			
	20.0139			

Table 2 (Cont'd)
HBV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
Other	1069.02 20.0136 20.0271 20.0137 2.0173 1.0073 1.0774 1039.06	SLDVSAAFY SWLSSLVPF SWPKFAVPNL SWWTSLNFL SYQHFRKLLI WFHHSCLTF WLWGMDIDPY WMMWWYGPSLY FLPSDFEFPSTI YMDDVVLGV FLPSDYFIPSV STLPEIYVVR FPIPSSWAF FPHICLAIFSL FPHICLAFAI IPITSSWAF IPIPMSWAF IPILSSWAF FPIVCLAFSY FPHICLAFAV	HBV pol 427 HBV ENV 334 HBV POL 392 HBV ENV 197 HBV POL 4 HBV NUIC 102 HBV adw CORI 416 HBV env 359	11Bv pol 427 11Bv ENV 334 11Bv POL 392 11Bv ENV 197 11Bv POL 4 11Bv NUIC 102 11Bv adw CORI 416 11Bv env 359
	924.14 1090.77 941.01 1083.02 1145.05 1145.11 1145.24 1145.06 1145.23 1145.07 1145.09 1145.10		HBV core 141-151 analog HBV ENV 313 analog HBV POL 541 analog HBV POL 541 analog HBV ENV 313 analog HBV ENV 313 analog HBV ENV 313 analog HBV POL 541 analog HBV POL 541 analog	11Bv 18-27 I _o var. 11Bv pol 538-546 sub 11Bc18-27 analog

Table 3
HCV derived HTL epitopes

Peptide	Sequence	Source	SEQ ID NO:
P98.03	AAYAAQGYKVLVLNPSVAATLGF ^{GAY}	HCV NS3 1242-1267	
P98.04	AAYAAQGYKVLVLNPSVAAT ^G	HCV NS3 1242	
P98.05	GYKVLVLNPSVAAT ^I LG ^{GAY}	HCV NS3 1248	
1283.21	GYKVLVLNPSVAAT ^G	HCV NS3 1248	
1283.20	GYKVLVLNPSVAAT ^G	HCV NS3 1253	
F134.08	GEGAVQWMNRLLIAFASRGNIIV GEGAVQWMNRLLIAFASRGNIIV	HCV NS4 1914-1935	
1283.44	MNRLIAFASRGNIHVS	HCV NS4 1921	
1283.16	SKGWLILLAPITAYAQ	HCV NS3 1025	
1283.55	GSSYGFQYSPPGQRVE	HCV NSS 2641	
F134.05	NFISGIQYLAGLSTLPGNPA	HCV NS4 1772	
1283.61	ASCLRKLGVPPLRVW	HCV NSS 2939	
1283.25	GRHLIFCHSKKKCDE	HCV NS3 1393	
35.0107	TVDFSLDPTFTIETT	HCV 1466	
35.0106	VVVVATDALMTGYTG	HCV 1437	

Table 4
HCV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A2	1090.18	FLLIADARV	HCV NS1/E2 728	
	1073.05	LJFNLGGWWV	HCV NS4 1812	
	1013.02	YLVAYQATIV	HCV NS3 1590	
	1013.1092	DLMGVIPLV	HCV Core 132	
	1090.22	RJJVFPLGIV	HCV NS5 2611	
	24.0075	VLYGGVLAA	HCV NS4 1666	
	24.0073	WMNRLLIAFA	HCV NS4 1920	
	1174.08	HMWNFISGIL	HCV NS4 1769	
	1073.06	ILAGYGAGV	HCV NS4 1851	
	24.0071	LFLFLLAADA	HCV NS1/E2 726	
A3	1073.07	YILPQRGPRL	HCV Core 35	
	1.0119	YLVTRHADV	HCV NS3 1136	
	1.0952	KTSERSQPR	HCV Core 51	
	1073.10	GVAGALVAFK	HCV NS4 1863	
	1.0123	LIFCHSKKK	HCV NS3 1391	
	1.0955	QLFTFSPPR	HCV E1 290	
	1073.11	RIGVVRATRK	HCV Core 43	
	1073.13	RMYVGGVEIR	HCV NS1/E2 635	
	24.0090	VAGALVAFK	HCV NS4 1864	
	F104.01	VGIYLLPNR	HCV NS5 3036	
B7	1145.12	LPGCSFSIF	HCV Core 168	
	29.0035	IPIFYGKAI	HCV 1378	
Other	1069.62	CYKXSSDLY	HCV NS3 1128	
	24.0092	PWAKIIMWNIF	HCV NS4 1765	
	13.0019	LSAFSLIISY	HCV NS5 2922	

Table 4 (Cont'd)
HCV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A3	24.0086	LGFGAYMSK	HCV NS3 1267	
	1174.21	RVCEKMALY	HCV NS5 2621	
	1174.16	WMNSTGRTK	HCV NS1/E2 557	
	1073.04	TLLIGRTPHLV	HCV NS3 1622	
B7	16.0012	HPVLYAQAA	HCV NS3 1588	
	15.0047	YPCIVNELL	HCV NS1/E2 623	
Other	24.0093	EVDGVRLIRY	HCV NS5 2129	
	3.0417	LTGGFADLMGY	HCV 126	
	1073.01	NIVDVQQLY	HCV E1 700	
	1.0509	GLSAFSLIISY	HCV NS5 2021	
	1073.17	MYVGDLLCGSVF	HCV E1 275	
	1073.18	MYVGGVBEHLR,	HCV NS1/E2 633	
	13.075	QYLAGLSTL	HCV NS4 1778	
	1145.13	PPGCSFSIF	HCV Core 168	
	1145.25	LPGCMFSIF	HCV Core 168	
	1292.24	LPGCSFSII	HCV Core 169	
	1145.14	LPVCSFSIF	HCV Core 168	
	1145.15	LPGCSFSYF	HCV Core 168	

Table 5
HIV derived IITL epitopes

Peptide	Sequence	Source	SEQ ID NO:
27.0313	GELYKRWIILGLNKIVRMYSPTSLID KRWIILGLNKIVRMYSPTSLID	HIV1 GAG 294-319 HIV gag 298-319	
27.0311	KIRWII.GLNKIVRMY	HIV1 GAG 298	
27.0354	GEIYKRWIILGN.KNI	HIV1 GAG 294	
27.0377	WEFVNNTPPVLVKLWYQ	HIV1 POL 596	
1280.03	QKQTKIQNFRVYYR	HIV1 POL 956	
27.0361	EKVYLAWWVPAHKGGG KVVYLAWWVPAHKGGG EKVYLAWWVPAHKGGG	HIV1 POL 711-726 HIV1 POL 712 HIV1 POL 711	
27.0304	PIVQNIQGQMVMHQASPRTLNA	HIV1 gag 165-186	
27.0297	QQGMVMHQASPRTLN QHLLQLTVWGKQLQ	HIV1 GAG 171 HIV1 ENV 729	
27.0344	SPAFQSSMTKILEP IKQFINNMWQEVGKAMY	HIV1 POL 335 HIV1 ENV 566	
F091.15	FRKYTAFTIPSINNE	HIV1 POL 303	
27.0341	HSNWVRAMASDFNLPP	HIV1 POL 758	
27.0364	KTAVQMAVFHNFKR	HIV1 POL 915	
27.0373	DRVHPVHAGPIAPGQMREPRGS AFSPEVPMFSALSEGATPQDLNTML AFSPEVPMFSALSEGATPQDL	HIV GAG 245 HIV gag 195-216 HIV gag 195-216 HIV gag 205	
200.06	SALSEGATPQDLNTML SPEVPMFSALSEGATPQDL	HIV gag 197 HIV gag 275 HIV gag 276	
27.0307	I.QEQIGWMINNIPPVGVLYKR	HIV VPU 31	
27.0310	QEQQGWMTNNNPPIV	HIV POL 874	
35.0135	YRKLRQRKIDRLID	HIV POL 674	
35.0131	WAGIKQEFQGIPYNPQ	HIV POL 619	
35.0127	EVNIVTDSQYALGII		
35.0125	AETFYVVDGAANRETAK		
35.0133	GAVVIQDNDIKVVP	HIV POL 989	

Table 6
HIV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A2	25.0148	MASDFNLPPV	HIV1 POL 70	
	1069.32	VLAEMSQV	HIV gag 397	
	1211.04	KLTPLCVT'L	HIV ENV 134	
	25.0062	KLVGKLNW'A	HIV1 POL 87	
	25.0039	LTFGWCFKL	HIV1 NEF 62	
	941.031	ILKEPVHGV	HIV1 pol 476-484	
	25.0035	MTNNNPPIPV	HIV1 GAG 34	
A3	25.0057	RILQQLLF1	HIV1 VPR 72	
	1.0944	AVFIHNFKR	HIV POL 1434	
	1.1056	KIQNPRVYRR	HIV POL 1474	
	1069.49	QMAVFHNFK	HIV pol 1432	
	966.0102	AIFQSSMTK	HIV pol 337	
	1150.14	MAVFHNFK	HIV pol 909	
	940.03	QYPLRPMTYK	HIV nef 73-82	
	25.0175	TTLFCASDAK	HIV1 ENV 81	
	1069.43	TVYYGVPVWK	HIV env 49	
	25.0209	VTKIGQQLK	HIV1 POL 65	
B7	1146.01	FPPVRQPVL	HIV nef 84-92	
	29.0060	IPIHYCAPA	HIV env 293	
	15.0073	FPISPIETV	HIV1 POL 171	
	29.0056	CPKVSFEP1	HIV env 285	
	29.0107	IPIYNPQSQQGVV	HIV1 pol 883	
	25.0151	CII.NIPIISHI	HIV1 POL 96	
	25.0143	LTFGWCFKLV	HIV1 NEF 62	
A2	25.0043	YTAFTIPS1	HIV1 POL 83	
	25.0055	AIRRLQQL	HIV1 VPR 76	
	25.0049	ALVEICTEM	HIV1 POL 52	
	25.0032	LLQLTVWGI	HIV1 ENV 61	
	25.0050	LVGPTIPVN1	HIV1 POL 100	
	25.0047	KAACCWWAGI	HIV1 POL 65	
	25.0162	KMIGGIGGGI	HIV1 POL 96	
	25.0052	RAMASDFNL	HIV1 POL 78	
	1211.09	SLLNATDIAV	HIV ENV 814	

Table 6 (Cont'd)
HIV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO.
A2	25.0041	TLNIPPISPI	HIV1 POL 96	
A3	1.0046	IWIWGIKTPK	HIV1'OL 1075	
	25.0064	MVHQQAISSPR	HIV1 GAG 45	
	1.0062	YLA WVPAIK	HIV POL 1227	
	1.0942	MTKILEPFR	HIV POL 859	
	25.0184	QMVIQQAISPR	HIV1 GAG 45	
	1069.48	AVFHINPKRK	HIV pol 1434	
	1069.44	KLAGRWPVK	HIV pol 1358	
	1069.42	KVYLA WVPAIK	HIV pol 1225	
	1.0024	NTPVFAIKK	HIV pol 752	
	25.0062	RIVELLGRR	HIV1 ENV 53	
	25.0095	TIKIGGQLK	HIV1 POL 65	
	25.0078	TLFCASDAK	HIV1 ENV 82	
	25.0104	VMIWQVDR	HIV1 VIF 83	
	1069.47	VTVVYYGVPVWK	HIV env 48	
B7	15.0268	YPLASLRSLF	HIV GAG 507	
	1292.13	HPVHAGPIA	HIV GAG 248	
	19.0044	VPLQLPPL	HIV con. REV 71	
Other	1.0431	EVNIVTDSQY	HIV POL 1187	
	1.0014	FRDYVDRFY	HIV GAG 298	
	25.0113	IWGCGSKLJ	HIV1 ENV 69	
	25.0127	IYETYGD'TW	HIV1 VPR 92	
	1069.60	IYQEPPFKNL	HIV pol 1036	
	2.0129	IYQYMDDLY	HIV pol 359	
	25.0128	PYNEWTLEI	HIV1 VPR 56	
	25.0123	PYNIPVFAI	HIV1'OL 74	
	1069.57	RYI.KDQQI.J	HIV env 2778	
	1069.58	RYLRDQQI.J	HIV env 2778	
	1069.59	TYQIYQEPf	HIV pol 1033	
	1069.27	VIYQYMDDLY	HIV pol 358	
	1069.26	VTVLDVDGDAY	HIV pol 265	
	25.0115	VWKEATTIL	HIV1 ENV 47	
	25.0218	VWKEATTILf	HIV1 ENV 47	
	25.0219	YMQATWIPPEW	HIV1 POL 96	

Table 6 (Cont'd)
HIV derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A2	I211.4	SLLNATAIAV	HIV MN gp160 814(a)	
	F105.21	AIFQRSMTK	HIV pol 337(a)	
	F105.17	AIFQSSMTK	HIV pol 337(a)	
	F105.02	GIFQSSMTK	HIV pol 337(a)	
	F105.03	AAFQSSMTK	HIV pol 337(a)	
	F105.04	AIAQSSMTK	HIV pol 337(a)	
	F105.05	AIFQASMTK	HIV pol 337(a)	
	F105.06	AIFQSAMTK	HIV pol 337(a)	
	F105.07	AIFQSSATK	HIV pol 337(a)	
	F105.08	AIFQSSMAK	HIV pol 337(a)	
A3	F105.09	FIFQSSMTK	HIV pol 337(a)	
	F105.11	SIFQSSMTK	HIV pol 337(a)	
	F105.12	AIFQCSMTK	HIV pol 337(a)	
	F105.16	AIFQCSMTK	HIV nef 84-92 analog	
	I145.03	FPVVRPQFPL	HIV nef 84-92(a)	
	I181.03	FPVVRPQVPL	HIV GAG 248	
	I292.14	HPVVAAGPIL	HIV POL 179	
	I292.09	FPISPIETI	HIV nef 84-92 analog	
	I145.02	FPVVTIPQVPL	HIV nef 84-92 analog	
	I145.22	FPVVRMQLQVPL	HIV nef 84-92(a)	
B7	I181.04	FPVVRPQVPM	HIV nef 84-92(a)	
	I181.01	FPVVRPQVPA	HIV nef 84-92(a)	
	I181.02	FPVVRPQVPV	HIV nef 84-92(a)	
	I181.05	FPVVRPQVPF	HIV nef 84-92(a)	
	I181.06	FPVVRPQVFW	HIV nef 84-92(a)	

Table 7
***P. falciparum* derived HTL epitopes**

Peptide	Sequence	Source	SEQ ID NO:
F125.04 1188.34 1188.16	RHNWVNHAVPLAMKLI HNWVNHAVPLAMKLI KSKYKLAATSVLAGL.I. LYNL.LIIFHNGKIKNS.E	Pf SSP2 61 Pf SSP2 62 Pf EXP1 71 Pf LSA1 13	
F125.02 27.0402	LVLILLIFHNGKIKNS.E LLIFHNGKIKNSE	Pf LSA1 13 Pf SSP2 512	
1188.32 27.0392	GLAYKFVVPGATPY SSVFNVNVNNSIGLIM	Pf CSP 410 Pf SSP2 223	
27.0417 27.0388	VKNVIGPFMKAVCVE MRKLAILSVSSFLFV	Pf CSP 2 Pf CSP 53	
27.0387	MNYYGKQENWYSLKK	Pf SSP2 494	
1188.38	KYKIAAGGIAGGLALL	Pf EXP1 82	
1188.13 27.0408 35.0171 35.0172	AGLLGNVSTVLLGGV QTNFKSLLRNLGSE PDSIQDSLKESRKLN KCNLYADSAWENVKN	Pf LSA1 94 Pf SSP2 165 Pf SSP2 211	

Table 8
P. falciparum derived CTL epitopes

Supertype	Peptide	Sequence	Source	SEQ ID NO:
A2	1167.21	FLLFFDLEFLV	Pf SSP2 14	
	1167.08	GILIMVLSFL	Pf CSP 425	
	1167.12	VIAAGLIGNV	Pf EXP1 80	
	1167.13	KILSVFELA	Pf EXP1 2	
	1167.10	GLLGNVSTV	Pf EXP1 83	
	1167.18	ILSVSSFLFV	Pf CSP 7	
	1167.19	VLLGGVGLVL	Pf EXP1 91	
A3	1167.36	LACAGLAYK	Pf SSP2 511	
	1167.32	QTNFKSSLR	Pf LSA1 194	
	1167.43	VTCCGNGIQVR	Pf CSP 375	
	1167.24	ALFFIILNK	Pf EXP1 10	
	1167.28	GVSENIFLK	Pf LSA1 105	
	1167.47	HNLSHNSYER	Pf LSA1 59	
	1167.51	LLACAGLAYK	Pf SSP2 510	
B7	1167.46	FILVNLLIHI	Pf LSA1 110	
	1101.03	MPLLETQLAI	Pf SHEBA 77	
	1167.61	TPYAGEPAPF	Pf SSP2 539	
	1167.14	FLLFFDLF	Pf SSP2 14	
	1167.15	FMKAIVCVER	Pf SSP2 230	
	1167.17	LIFFDLFLV	Pf SSP2 15	
	1167.09	LLMDCSGSI	Pf SSP2 51	
B7	19.0051	VIIJCCVGIV	Pf EXP1 91	
	16.0245	IPIYGIRINI	Pf SSP2 126	
	16.0040	IQDLEENIY	Pf LSA1 1794	
	1167.54	FVEALFQEVY	Pf CSP 15	
	1167.53	FYFILVNL	Pf LSA1 9	
	1167.56	KYKLAISVL	Pf EXP1 73	
	15.0184	KYLVIVFLI	Pf SSP2 8	
Other	16.0130	LPSENERGY	Pf LSA1 1663	
	16.0077	PSDGKCNLY	Pf SSP2 207	
	1167.57	PSENERGY	Pf LSA1 1664	
	1167.55	PYAGEPAPF	Pf SSP2 528	
		YYIPHQSLL	Pf LSA1 1671	

Table 9. Activation of T Cell Proliferation by Expression
Vectors Encoding MHC Class II Epitopes Fused to MHC
Class II Targeting Sequences

5

	Immunogen	Stimulating Peptide ¹		
		PADRE	OVA 323	CORE 128
10	peptide - CFA ²	3.0 (1.1)	2.7 (1.2)	3.2 (1.4)
	pEP2.(PAOS).(-)	-	-	-
	pEP2.(AOS).(-)	5.6 (1.8)	-	-
	pEP2.(PAOS).(sigTh)	5.0 (2.9)	-	2.6 (1.5)
	pEP2.(PAOS).(IgαTh)	5.6 (2.1)	-	3.0 (1.6)
	pEP2.(PAOS).(LampTh)	3.8 (1.7)	-	3
	pEP2.(PAOS).(IiTh)	5.2 (2.0)	3.2 (1.5)	3.7 (1.5)
	pEP2.(PAOS).(H2M)	3.3 (1.3)	-	2.8

¹Geometric mean of cultures with SI ≥ 2.

²Proliferative response measured in the lymph node.

20

Table 10
CTL Epitopes in cDNA Minigene
Immunogenicity In Vivo (IFA)

Epitope	Sequence	MHC Restrict.	MHC Binding Affinity [IC30% (nM)]	No. CTL-Positive Cultures	CTL Response
					(Geo. Mean x/ \pm SD) ^b
HBV Core 18	FLPSDFFPSV	A2.1	3	6 / 6	73.0 (1.1)
HBV Env 335	WLSLLVPFV	A2.1	5	4 / 6	5.3 (1.6)
HBV Pol 455	GLSRYVVARL	A2.1	76	ND ^c	ND
HIV Env 120	KLTPLCVTL	A2.1	102	2 / 5	6.4 (1.3)
HIV Pol 476	ILKEPVHGV	A2.1	192	2 / 5	15.2 (2.9)
HBV Pol 551-A	YMDDVVLGA	A2.1	200	0 / 6	-
HBV Pol 551-V	YMDDVVLGV	A2.1	5	6 / 6	8.2 (2.3)
HIV Env 49	TVYYGVPVWK	A11	4	28 / 33	13.4 (3.1)
HBV Core 141	STLPETTVVRR	A11	4	6 / 6	12.1 (2.6)
HBV Pol 149	HTLWKAGILYK	A11	14	6 / 6	13.1 (1.2)

a Peptide tested in HLA-A2.1/K^b H-2^{b₁₂} transgenic mice by co-immunizing with a T helper cell peptide in IFA.

5 b Geometric mean CTL response of positive cultures.

c ND, not done.

Table 11
Summary of Immunogenicity of pMin.1 DNA construct in HLA A2.1/K^b transgenic mice

Epitope	CTL Response ^a	
	No. Positive Cultures/Total ^b	Geo. Mean Response Positive Cultures [$\times \pm SD$] ΔLU
HBV Core 18	9 / 9	455.5 [2.2]
HIV Env 120	12 / 12	211.9 [3.7]
HBV Pol 551-V	9 / 9	126.1 [2.8]
HBV Pol 455	12 / 12	738.6 [1.3]
HIV Pol 476	11 / 11	716.7 [1.5]
HBV Env 335	12 / 12	43.7 [1.8]
HBV Core 18 (Theradigm) ^c	10 / 10	349.3 [1.8]

^a Mice were immunized with pMin.1 DNA or Theradigm-HBV lipopeptide and CTL activity in splenocyte cultures was determined after in vitro stimulation with individual peptide epitopes. Results from four independent experiments are shown.

^b See Example V, Materials and Methods for definition of a CTL-positive culture.

^c Response of mice immunized with Theradigm-HBV lipopeptide containing the HBV Core 18 epitope.

Table 12
Summary of immunogenicity
in HLA A11/K^b transgenic mice

Epitope	CTL Response ^a	
	No. Positive Cultures/Total ^b	Geo. Mean Response Positive Cultures [x/ \pm SD]
Δ LU		
HBV Core 141	5/9	128.1 [1.6]
HBV Pol 149	6/9	267.1 [2.2]
HIV Env 43	9/9	40.1 [2.9]

- ^a Mice were immunized with pMin.1 DNA and CTL activity in splenocyte cultures was determined after in vitro stimulation with individual A11-restricted epitopes. The geometric mean CTL response from three independent experiments are shown.
- ^b 5 Definition of a CTL-positive culture is described in Example V, Materials and Methods.

WHAT IS CLAIMED IS:

- 1 1. An expression vector comprising a promoter operably linked to a
2 first nucleotide sequence encoding a major histocompatibility (MHC) targeting sequence
3 fused to a second nucleotide sequence encoding two or more heterologous peptide
4 epitopes, wherein the heterologous peptide epitopes comprise two HTL peptide epitopes
5 or a CTL peptide epitope and a universal HTL peptide epitope.
- 1 2. The expression vector of claim 1, wherein the heterologous peptide
2 epitopes comprise two or more heterologous HTL peptide epitopes.
- 1 3. The expression vector of claim 1, wherein the heterologous peptide
2 epitopes comprise a CTL peptide epitope and a universal HTL peptide epitope.
- 1 4. The expression vector of claim 2, wherein the heterologous peptide
2 epitopes further comprise one or more CTL peptide epitopes.
- 1 5. The expression vector of claim 3, wherein the heterologous peptide
2 epitopes further comprise two or more CTL peptide epitopes.
- 1 6. The expression vector of claim 3, wherein the heterologous peptide
2 epitopes further comprise two or more HTL peptide epitopes.
- 1 7. The expression vector of claim 2, wherein one of the HTL peptide
2 epitopes is a universal HTL epitope.
- 1 8. The expression vector of claim 3 or 7, wherein the universal HTL
2 epitope is a pan DR epitope.
- 1 9. The expression vector of claim 8, wherein the pan DR epitope has
2 the sequence AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38).
- 1 10. The expression vector of claim 1, wherein the peptide epitopes are
2 hepatitis B virus epitopes, hepatitis C virus epitopes, human immunodeficiency virus
3 epitopes, human papilloma virus epitopes, MAGE epitopes, PSA epitopes, PSM epitopes,
4 PAP epitopes, p53 epitopes, CEA epitopes, Her2/neu epitopes, or *Plasmodium* epitopes.

1 11. The expression vector of claim 10, wherein the peptide epitopes
2 each have a sequence selected from the group consisting of the peptides depicted in
3 Tables 1-8.

1 12. The expression vector of claim 11, wherein at least one of the
2 peptide epitopes is an analog of a peptide depicted in Tables 1-8.

1 13. The expression vector of claim 1, wherein the MHC targeting
2 sequence comprises a region of a polypeptide selected from the group consisting of the Ii
3 protein, LAMP-I, HLS-DM, HLA-DO, H2-DO, influenza matrix protein, hepatitis B
4 surface antigen, hepatitis B virus core antigen, Ty particle, Ig- α protein, Ig- β protein, and
5 Ig kappa chain signal sequence.

1 14. The expression vector of claim 1, wherein the expression vector
2 further comprises a second promoter sequence operably linked to a third nucleotide
3 sequence encoding one or more heterologous HTL or CTL peptide epitopes.

1 15. The expression vector of claim 1, wherein the vector comprises
2 pMin1 or pEP2.

1 16. The expression vector of claim 3 or 4, wherein the CTL peptide
2 epitope comprises a structural motif for an HLA supertype, whereby the peptide CTL
3 epitope binds to two or more members of the supertype with an affinity of greater than
4 500 nM.

1 17. The expression vector of claim 4 or 5, wherein the CTL peptide
2 epitopes have structural motifs that provide binding affinity for more than one HLA allele
3 supertype.

1 18. A method of inducing an immune response *in vivo* comprising
2 administering to a mammalian subject an expression vector comprising a promoter
3 operably linked to a first nucleotide sequence encoding a major histocompatibility (MHC)
4 targeting sequence fused to a second nucleotide sequence encoding two or more
5 heterologous peptide epitopes, wherein the heterologous peptide epitopes comprise two
6 HTL peptide epitopes or a CTL peptide epitope and a universal HTL peptide epitope.

1 19. The method of claim 18, wherein the heterologous peptide epitopes
2 comprise two or more heterologous HTL peptide epitopes.

1 20. The method of claim 18, wherein the heterologous peptide epitopes
2 comprise a CTL peptide epitope and a universal HTL peptide epitope.

1 21. The method of claim 19, wherein the heterologous peptide epitopes
2 further comprise one or more CTL peptide epitopes.

1 22. The method of claim 20, wherein the heterologous peptide epitopes
2 further comprise two or more CTL peptide epitopes.

1 23. The method of claim 20, wherein the heterologous peptide epitopes
2 further comprise two or more HTL peptide epitopes.

1 24. The method of claim 19, wherein the HTL peptide epitope is a
2 universal HTL epitope.

1 25. The method of claim 20 or 24, wherein the universal HTL epitope
2 is a pan DR epitope.

1 26. The method of claim 25, wherein the pan DR epitope has the
2 sequence AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38).

1 27. The method of claim 18, wherein the peptide epitopes are hepatitis
2 B virus epitopes, hepatitis C virus epitopes, human immunodeficiency virus epitopes,
3 human papilloma virus epitopes, MAGE epitopes, PSA epitopes, PAP epitopes, PSM
4 epitopes, p53 epitopes, CEA epitopes, Her2/neu epitopes, or *Plasmodium* epitopes.

1 28. The method of claim 27, wherein the peptide epitopes each have a
2 sequence selected from the group consisting of the peptides depicted in Tables 1-8.

1 29. The method of claim 28, wherein least one of the peptide epitopes
2 is an analog of a peptide depicted in Tables 1-8.

1 30. The method of claim 18, wherein the MHC targeting sequence
2 comprises a region of a polypeptide selected from the group consisting of the Ii protein,
3 LAMP-I, HLS-DM, HLA-DO, H2-DO, influenza matrix protein, hepatitis B surface

4 antigen, hepatitis B virus core antigen, Ty particle, Ig- α protein, Ig- β protein, and Ig
5 kappa chain signal sequence.

1 31. The method of claim 18, wherein the expression vector further
2 comprises a second promoter sequence operably linked to a third nucleotide sequence
3 encoding one or more heterologous HTL or CTL peptide epitopes.

1 32. The method of claim 18, wherein the vector comprises pMin.1 or
2 pEP2.

1 33. The method of claim 20 or 21, wherein the CTL peptide epitope
2 comprises a structural motif for an HLA supertype, whereby the peptide epitope binds to
3 two or more members of the supertype with an affinity of greater than 500 nM.

1 34. The method of claim 21 or 22, wherein the CTL peptide epitopes
2 have structural motifs that provide binding affinity for more than one HLA allele
3 supertype.

1 35. A method of inducing an immune response *in vivo* comprising
2 administering to a mammalian subject an expression vector comprising a promoter
3 operably linked to a first nucleotide sequence encoding a major histocompatibility (MHC)
4 targeting sequence fused to a second nucleotide sequence encoding a heterologous human
5 HTL peptide epitope.

1 36. The method of claim 35, wherein the second nucleotide sequence
2 further comprises two or more heterologous HTL peptide epitopes.

1 37. The method of claim 35, wherein the second nucleotide sequence
2 further comprises one or more heterologous CTL peptide epitopes.

1 38. The method of claim 35, wherein the HTL peptide epitope is a
2 universal HTL peptide epitope

1 39. The method of claim 38, wherein the universal HTL epitope is a
2 pan DR epitope.

1 40. The method of claim 39, wherein the pan DR epitope has the
2 sequence AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38).

1 41. The method of claim 37, wherein the HTL and CTL peptide
2 epitopes are hepatitis B virus epitopes, hepatitis C virus epitopes, human
3 immunodeficiency virus epitopes, human papilloma virus epitopes, MAGE epitopes, PSA
4 epitopes, PAP epitopes, PSM epitopes, p53 epitopes, CEA epitopes, Her2/neu epitopes,
5 or *Plasmodium* epitopes.

1 42. The method of claim 41, wherein the peptide epitopes each have a
2 sequence selected from the group consisting of the peptides depicted in Tables 1-8.

1 43. The method of claim 42, wherein at least one of the peptide
2 epitopes is an analog of a peptide depicted in Tables 1-8.

1 44. The method of claim 35, wherein the MHC targeting sequence
2 comprises a region of a polypeptide selected from the group consisting of the Ii protein,
3 LAMP-I, HLS-DM, HLA-DO, H2-DO, influenza matrix protein, hepatitis B surface
4 antigen, hepatitis B virus core antigen, Ty particle, Ig- α protein, Ig- β protein, and Ig
5 kappa chain signal sequence.

1 45. The method of claim 35, wherein the expression vector further
2 comprises a second promoter sequence operably linked to a third nucleotide sequence
3 encoding one or more heterologous HTL or CTL peptide epitopes.

1 46. The method of claim 37, wherein the CTL peptide epitope
2 comprises a structural motif for an HLA supertype, whereby the peptide epitope binds to
3 two or more members of the supertype with an affinity of greater than 500 nM.

1 47. The method of claim 37, wherein the CTL peptide epitopes have
2 structural motifs that provide binding affinity for more than one HLA allele supertype.

1 48. A method of assaying the human immunogenicity of a human T
2 cell peptide epitope *in vivo* in a non-human mammal, comprising the step of
3 administering to the non-human mammal an expression vector comprising a promoter
4 operably linked to a first nucleotide sequence encoding a heterologous human CTL or
5 HTL peptide epitope.

1 49. The method of claim 48, wherein the first nucleotide sequence
2 encodes two or more heterologous CTL or HTL peptide epitopes.

1 50. The method of claim 48, wherein the non-human mammal is a
2 transgenic mouse that expresses a human HLA allele.

1 51. The method of claim 50, wherein the human HLA allele is selected
2 from the group consisting of A11 and A2.1.

1 52. The method of claim 48, wherein the expression vector further
2 comprise a second nucleotide sequence encoding a major histocompatibility (MHC)
3 targeting sequence.

1 53. The method of claim 48, wherein the HTL peptide epitope is a
2 universal HTL epitope.

1 54. The method of claim 53, wherein the universal HTL epitope is a
2 pan DR epitope.

1 55. The method of claim 54, wherein the pan DR epitope has the
2 sequence AlaLysPheValAlaAlaTrpThrLeuLysAlaAlaAla (SEQ ID NO:38).

1 56. The method of claim 48, wherein the CTL or HTL peptide epitopes
2 are hepatitis B virus epitopes, hepatitis C virus epitopes, human immunodeficiency virus
3 epitopes, human papilloma virus epitopes, MAGE epitopes, PSA epitopes, PSM epitopes,
4 PAP epitopes, p53 epitopes, CEA epitopes, Her2/neu epitopes, or *Plasmodium* epitopes.

1 57. The method of claim 56, wherein the CTL or HTL peptide epitopes
2 each have a sequence selected from the group consisting of the peptides depicted in
3 Tables 1-8.

1 58. The method of claim 57, wherein at least one of the peptide
2 epitopes is an analog of a peptide depicted in Tables 1-8.

1 59. The method of claim 52, wherein the MHC targeting sequence
2 comprises a region of a polypeptide selected from the group consisting of the Ii protein,

3 LAMP-I, HLS-DM, HLA-DO, H2-DO, influenza, hepatitis B virus core antigen, Ty
4 particle, Ig- α protein, Ig- β protein, and Ig kappa chain signal sequence.

1 60. The method of claim 48, wherein the expression vector further
2 comprises a second promoter sequence operably linked to a third nucleotide sequence
3 encoding one or more heterologous human CTL or HTL peptide epitopes.

1 61. The method of claim 48, wherein the vector comprises pMin.1 or
2 pEP2.

1 62. The method of claim 48, wherein the CTL peptide epitope has a
2 structural motif that provides binding affinity for an HLA allele supertype.

1 63. The method of claim 49, wherein the CTL peptide epitopes have
2 structural motifs that provide binding affinity for more than one HLA allele supertype.

1 64. The method of claim 48, wherein the expression vector comprises
2 both HTL and CTL peptide epitopes.

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGATGACCAACGCGACCTCATCTCTAACCATGAGCAATTGCCCATACTGGGCA						
CGATCGCGCGGTGGTACCTACTGGTTGCGCTGGAGTAGAGATTGGTACTCGTTAACGGGTATGACCCGT						
M D D Q R D L I S N H E Q L P I L G >						
80	90	100	110	120	130	140
*	*	*	*	*	*	*
ACCGCCCTAGAGAGCCAGAAAGGTCAGCCGTTGGAGCTCTGTACACCGGGTCTTCTGTCCTGGTGGCTCT						
TGGCGGGATCTCTCGGTCTTCCACGTGGCACCTGAGACATGTGGCCACAAAGACAGGACCACCGAGA						
N R P R E P E R C S R G A L Y T G V S V L V A L >						
150	160	170	180	190	200	210
*	*	*	*	*	*	*
GCTCTGGCTGGCAGGCCACCTGCTACTTCTGTACCGAACAGGGCCGCTAGACAAGCTGACC						
CGAGAACCGACCCGTCGGTGGTACGAATGAAGGACATGGTCGTTGTCGGCGGATCTGTCGACTGG						
L L A G Q A T T A Y F L Y Q Q Q G R L D K L T >						
220	230	240	250	260	270	280
*	*	*	*	*	*	*
ATCACCTCCCAGAACCTGCAACTGGAGAGGCCTTCGATGAAGCTTCCGAAATCTGCCAACCTGTGGCA						
TAGTGGAGGTCTGGACGTTGACCTCTCGGAACGCTACTTCAAGGCTTTAGACGGTTGGACACCGGT						
I T S Q N L Q L E S L R M K L P K S A K P V A >						
290	300	310	320	330	340	350
*	*	*	*	*	*	*
AGTTCGTGGCTGCCTGGACCCCTGAAAGGCTGCCCTATGTCCATGGATAACATGCTCCTGGGCTGTGAA						
TCAAGCACCGACGGACCTGGACTTCCGACGGCATACAGGTACCTATTGTACGAGGAACCCGGACACTT						
K F V A A W T L K A A A M S M D N M L L G P V K >						
360	370	380	390	400	410	420
*	*	*	*	*	*	*
GAACGTTACCAAGTACGGCAACATGACCCAGGGCATGTGATGCATCTGTCACGGAGGTCTGGACCCCTG						
CTTGCAATGGTTCATGCCGTTGACTGGTCTGGTACACTACGTAGACGAGTGCTCCAGACCTGGGAC						
N V T K Y G N M T Q D H V M H L L T R S G P L >						
430	440	450	460	470	480	490
*	*	*	*	*	*	*
GAGTACCCCGAGCTGAAGGGGACCTTCCCAGAGAACCTGAAAGCATCTTAAGAACCTCCATGGATGGCGTGA						
CTCATGGCGCTCGACTTCCCTGAAAGGTCTTGTACCTCGTAGAACCTTGTGAGGTACCTACCGCACT						
E Y P Q L K G T F P E N L K H L K N S M D G V >						
500	510	520	530	540	550	560
*	*	*	*	*	*	*
ACTGGAAAGATCTTCGAGAGCTGGTGAAGCAGTGGCTTGTGAGATGAGCAAGAACCTCCCTGGAGGA						
TGACCTCTAGAAGCTCTCGACCTACTCGTAGGAGAACAAACTCTACTCGTTCTGAGGGACCTCCT						
N W K I F E S W M K Q W L L F E M S K N S L E E >						
570	580	590	600	610	620	630
*	*	*	*	*	*	*
GAAGAAGCCCCACCGAGGCTCCACCTAAAGAGCCACTGGACATGGAGACCTATCTTCTGGCCTGGGAGTG						
CTCTCTGGGTGGCTCGAGGTGGATTCTCGGTACCTCTGGATAGAAGACCGGACCCCTCAC						
K K P T E A P P K E P L D M E D L S S G L G V >						
640	650	660				
*	*	*	*	*	*	*
ACCAGGCAGGAACCTGGGTCAAGTCACCCCTGTGAGGTAC						
TGGTCCGTCTTGACCCAGTTCAAGTGGACACTCCATGG						
T R Q E L G Q V T L * >						

FIGURE 1

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGATGACCAACCGCAGCTCATCTAACCATGAGCAATTGCCATACTGGCA						
CGATCGCGGGCGGTGGTACCTACTGGTTGCCTGGAGTAGAGATTGGTACTCGTTAACGGGTATGACCGT						
M D D Q R D L I S N H E Q L P I L G >						
80	90	100	110	120	130	140
*	*	*	*	*	*	*
ACCGCCCTAGAGAGCCAGAAAGGTGCAGCCGTGGAGCTGTACACCGGTGTTCTGTCCTGGTGGCTCT						
TGGCGGGATCTCTCGGTCTTCCACGTCCGGCACCTCGAGACATGTGGCCACAAAGACAGGACCACCGAGA						
N R P R E P E R C S R G A L Y T G V S V L V A L >						
150	160	170	180	190	200	210
*	*	*	*	*	*	*
GCTCTGGCTGGGCAGGCCACCACTGCTTACCTCCTGTACCAAGCAACAGGGCCGCTAGACAAGCTGACC						
CGAGAACCGACCCGTCCGGTGGTGACGAATGAAGGACATGGTCGTTGTCGGCGGATCTGTTGACTGG						
L L A G Q A T T A Y F L Y Q Q Q G R L D K L T >						
220	230	240	250	260	270	280
*	*	*	*	*	*	*
ATCACCTCCCAGAACCTGCACTGGAGAGCCTTCGCATGAAGCTTATCAGCCAGGCTGTGCACGCCGCTC						
TAGTGGAGGGTCTTGGACCTCTCGGAAGCGTACTTCGAATAGTCGGTCCGACACGTGCGGCGAG						
I T S Q N L Q L E S L R M K L I S Q A V H A A >						
290	300	310	320	330	340	350
*	*	*	*	*	*	*
ACGCCGAATCAACGAAGCTGGAAGAACCCCTCCAGCTTATGCCCTCCAACGCTCCTATCCTGTTCTT						
TGCCTTCTGCTTCGACCTCTGGGGAGGTCGAATAGCGGGAGGTTGCGAGGATAGGACAAGAA						
H A E I N E A G R T P P A Y R P P N A P I L F F >						
360	370	380	390	400	410	420
*	*	*	*	*	*	*
TCTGGTGACCGAGAACCTGACAATCCCCAGTCCTGGACGCCAGTTCTGGCTGCCCTGGACCCCTGAAG						
AGACGACTGGTCTTAGGACTGTTAGGGGTCAGGGACCTCGGGTTCAAGCACCGACGGACCTGGACCTTC						
L L T R I L T I P Q S L D A K F V A A W T L K >						
430						
*	*	*	*	*	*	*
GCTGCCGCTTGAGGTACC						
CGACGGCGAACCTCCATGG						
A A A * >						

FIGURE 2

10 20 30 40 50 60 70
 * * * * * * *
 GCTAGCGCCGCCACCATGGATGACCAACGCGACCTCATCTCTAACCATGAGCAATTGCCCATACTGGCA
 CGATCGCGCGGTGGTACCTACTGGTTGGCTGGAGTAGAGATTGGTACTCGTTAACGGGTATGACCCGT
 M D D Q R D L I S N H E Q L P I L G>
 80 90 100 110 120 130 140
 * * * * * * *
 ACCGGCCCTAGAGAGGCCAGAAAGGTGCAGCCGGAGCTCTGTACACCGGTGTTCTGTCCTGGTGGCTCT
 TGGCGGGATCTCTCGGTCTTCACGGCACCTCGAGACATGTGGCACAAAGACAGGACCACCGAGA
 N R P R E P E R C S R G A L Y T G V S V L V A L>
 150 160 170 180 190 200 210
 * * * * * * *
 GCTCTTGCTGGGCAGGCCACCTGCTTACTCTGTACAGCAACAGGGCCCTAGACAAGCTGACC
 CGAGAACCGACCCGTCGGTGGTGGTGAAGCATGGTGTGTCGGCGGAGCTGTCGACTGG
 L L A G Q A T T A Y F L Y Q Q Q G R L D K L T>
 220 230 240 250 260 270 280
 * * * * * * *
 ATCACCTCCCAGAACCTGCAACTGGAGAGCCTTCGATGAAGCTTATCAGCCAGGCTGTGCACGCCGCTC
 TAGTGGAGGGTCTTGACGTTGACCTCTCGGAAGCGTACTTCGAATAGTCGGTCCGACACGTGGCGGAG
 I T S Q N L Q L E S L R M K L I S Q A V H A A>
 290 300 310 320 330 340 350
 * * * * * * *
 ACGCCGAAATCAACGAAGCTGGAGAACCCCCCTCCAGCTTATCGCCCTCCAACGCTCTATCCTGTTCTT
 TGCGGCTTAGTTGCTTCGACCTCTTGGGGAGGTGCAATAGCGGGAGGTTGCGAGGATAGGACAAGAA
 H A E I N E A G R T P P A Y R P P N A P I L F F>
 360 370 380 390 400 410 420
 * * * * * * *
 TCTGCTGACCAGAACCTGACAACTCCCCAGTCCCTGGACGCCAGTCGTGGCTGCCCTGGACCCCTGAAG
 AGACGACTGGCTTAGGACTGTTAGGGGTCAAGGACCTGCGGTTCAAGCACCGACGGACCTGGACTTC
 L L T R I L T I P Q S L D A K F V A A W T L K>
 430 440 450 460 470 480 490
 * * * * * * *
 GCTGCCGCTATGTCATGGATAACATGCTCTGGGCTGTGAAGAACGTTACCAAGTACGGAACATGA
 CGACGGCGATACAGGTACCTATTGAGGAACCCGGACACTCTTGAATGGTTATGCCGTTGACT
 A A A M S M D N M L L G P V K N V T K Y G N M>
 500 510 520 530 540 550 560
 * * * * * * *
 CCCAGGACCATGTGATGCATCTGTCACGAGGTGGACCCCTGGAGTACCCGAGCTGAAGGGGACCTT
 GGGTCTGGTACACTACGTAGACGAGTGCTCCAGACCTGGGACCTCATGGCGTCACTTCCCTGGAA
 T Q D H V M H L L T R S G P L E Y P Q L K G T F>
 570 580 590 600 610 620 630
 * * * * * * *
 CCCAGAGAACATGAAACTCCATGGATGGCTGAACCTGAGAAGATCTCGAGAGCTGGATG
 GGGTCTTAGACTTCGTTAGAATTCTGAGGTACCTACCGCACTTGACCTTCTAGAAGCTCTGACCTAC
 P E N L K H L K N S M D G V N W K I F E S W M>

FIGURE 3

640 650 660 670 680 690 700
* * * * * * * * * * *
AAGCAGTGGCTCTTGTGAGATGAGCAAGAACTCCCTGGAGGGAGAAGAAGGCCACCGAGGCTCCACCTA
TTCGTCAACCGAGAACAAACTCTACTCGTTCTTGAGGGACCTCCTCTTCGGGTGGCTCCGAGGTGGAT
K Q W L L F E M S K N S L E E K K P T E A P P>

710 720 730 740 750 760 770
* * * * * * * * * * * *
AAGAGCCACTGGACATGGAGACCTATCTTCTGGCTGGGAGTGAACCGAGGAACCTGGGTCAAGTCAC
TTCTCGGTGACCTGTACCTCTGGATAGAAGACCGGACCCCTCACTGGTCCGTCTTGACCCAGTTCAAGTG
K E P L D M E D L S S G L G V T R Q E L G Q V T>

780
* *
CCTGTGAGGTACC
GGACACTCCATGG
L * >

FIGURE 3 CONTINUED

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCTGTGGGTGCCG						
CGATCGCGCGGTGGTACCCCTACGTCCACGTCTAGGTCTCGGACAAAGACGAGGAGGACACCCACGGC						
M	G	M	Q	V	L	P>
80	90	100	110	120	130	140
*	*	*	*	*	*	*
GGTCCAGAGGAATCAGCCAGGTGTGCAGGCCGTCACGCCGAAATCAACGAAGCTGGAAGAACCCCTCC						
CCAGGTCTCCTTAGTCGGTCCGACACGTGCGGCGAGTGCGGCTTAGTTGCTCGACCTCTTGGGGAGG						
G	S	R	G	I	S	P>
150	160	170	180	190	200	210
*	*	*	*	*	*	*
AGCTTATCGCCCTCCAACGCTCCTATCCTGTTCTCTGCTGACCAGAACCTGACAATCCCCAGTCC						
TCGAATAGCGGGAGGTTTGCAGGATAGGACAAGAAAGACGACTGGTCTTAGGACTGTTAGGGGTCAAGG						
A	Y	R	P	P	N	S>
220	230	240	250	260	270	280
*	*	*	*	*	*	*
CTGGACGCCAAGTCGTGGCTGCCCTGACCTGAAGGCTGCCGCTAACAACATGTTGATCCCCATTGCTG						
GACCTGCGGTTCAAGCACCGACGGACCTGGACTTCCGACGGCGATTGTTGACAACTAGGGTAACGAC						
L	D	A	K	F	V	A>
290	300	310	320	330	340	350
*	*	*	*	*	*	*
TGGGCGGTGCCCTGGCAGGGCTGGTCCTCATCGTCCTCATTCCTACCTCATTGGCAGGAAGAGGGACTCA						
ACCCGCCACGGGACCGTCCCACCAAGGAGTAGCAGGAGAACGGATGGAGTAACCGTCCTCTCCTCAGT						
V	G	G	A	L	A	H>
360	370					
*	*	*	*	*		
CGCCGGCTATCAGACCATCTAGGGTACC						
GCGGCCGATAGTCGGTAGATCCCATGG						
A	G	Y	Q	T	I	>

FIGURE 4

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGCTGCACTCTGGCTGCTGCTGGTCTCAGTCTGCACGTATGGGGATCA						
CGATCGCGCGGTGGTACCGACGTGAGACCGACGACGACCAGGAGTCAGACGTGACATAACCCCTAGT						
M A A L W L L L V L S L H C M G I >						
80	90	100	110	120	130	140
*	*	*	*	*	*	*
GCCAGGCTGTGCACGCCGCTACGCCGAAATCAACGAAGCTGGAAGAACCCCTCCAGCTTATCGCCCTCC						
CGGTCCGACACGTGCGGCGAGTGCCTTAGTTCGACCTCTGGGAGGTGAAATAGCGGGAGG						
S Q A V H A A H A E I N E A G R T P P A Y R P P >						
150	160	170	180	190	200	210
*	*	*	*	*	*	*
AAACGCTCCTATCCTGTTCTCTGCTGACCAGAATCCTGACAATCCCCAGTCCCTGGACGCCAAGTTC						
TTTGGCAGGATAGGACAAGAAAGACGACTGGCTTAGGACTGTTAGGGGTCAAGGACCTGCGGTTCAAG						
N A P I L F F L L T R I L T I P Q S L D A K F >						
220	230	240	250	260	270	280
*	*	*	*	*	*	*
GTGGCTGCCTGGACCCCTGAAGGCTGCCGCTAAGGTCTCTGTGTCTGCAGCCACCCCTGGGCTGGCTTC						
CACCGACGGACCTGGACTTCCGACGGCATTCCAGAGACACAGACGTGGTGGGACCCGGACCCGAAGT						
V A A W T L K A A A K V S V S A A T L G L G F >						
290	300	310	320	330	340	350
*	*	*	*	*	*	*
TCATCTTCTGTGTTGGCTTCAGATGGCGCAAGTCTCATTCTCCAGCTACACTCCTCTCCCTGGATC						
AGTAGAAGACACAACCGAAGAAGTCTACCGCGTTCAAGAGTAAGGAGGTGATGTGAGGGAGAGGGACCTAG						
I I F C V G F F R W R K S H S S S Y T P L P G S >						
360	370	380				
*	*	*	*	*	*	*
CACCTACCCAGAAGGACGGCATTAGGGTACC						
GTGGATGGGTCTCTGCCGTAAATCCCATGG						
T Y P E G R H * >						

FIGURE 5

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGCGCTGGGAGGGCCCCCTGGGTGGCTCTGTTGGTGAACCTCATGAGGC						
CGATCGCGCGGTGGTACCCCGCACCCCTCCGGGGGACCCACCACCGAGACAAACCACTTGGAGTACTCCG						
M G A G R A P W V V A L L V N L M R >						
80	90	100	110	120	130	140
*	*	*	*	*	*	*
TGGATTCCATCAGCCAGGTGTGCACGCCCTCACGCCAAATCAACGAAGCTGGAAGAACCCCTCCAGC						
ACCTAAGGTAGTCGGTCCGACACGTGCAGTGAGTGGCTTAGTTGCTTCGACCTTCTGGGGAGGTGCG						
L D S I S Q A V H A A H A E I N E A G R T P P A >						
150	160	170	180	190	200	210
*	*	*	*	*	*	*
TTATCGCCCTCAAACGCTCTATCCTGTTCTTCTGCTGACCAGAACATCCTGACAATCCCCAGTCCTG						
AATAGCGGGAGGTTTGCAGGATAGGACAGAAAGACGACTGGTCTTAGGACTGTTAGGGGTCAGGGAC						
Y R P P N A P I L F F L L T R I L T I P Q S L >						
220	230	240	250	260	270	280
*	*	*	*	*	*	*
GACGCCAAGTTCGTGGCTGGACCTGAAAGGCTGCCCTATACTGAGTGGAGCTGCAGTGGTCTGC						
CTGGGTTCAAGCACCGACGGACCTGGACTTCCGACGGCATATGACTCACCTCGACGTACAAGGACG						
D A K F V A A W T L K A A A I L S G A A V F L >						
290	300	310	320	330	340	350
*	*	*	*	*	*	*
TTGGGCTGATTGTCTTCTGGTGGGGGTTATCCATCTCAAGGCTCAGAAAAGCATCTGTTGGAGACTCA						
AACCCGACTAACAGAAGGACCACCCCAACAATAGGTAGAGTTCGAGTCCTTGTAGACACCTCTGAGT						
L G L I V F L V G V V I H L K A Q K A S V E T Q >						
360	370	380	390	400	410	420
*	*	*	*	*	*	*
GCCTGGCAATGAGAGTAGGTCCCGGATGATGGAGCGGCTAACCAAGTTCAAGGCTGGACCGGGACATGTC						
CGGACCGTTACTCTCATCCAGGGCTACTACCTCGCGATTGGTCAAGTTCGACCTGGCCCTGTACAG						
P G N E S R S R M M E R L T K F K A G P G H V >						
430						
*	*	*	*	*	*	*
ACATGAGGTACC						
TGTACTCCATGG						
T * >						

FIGURE 6

10 * * * * 20 * * * * 30 * * * * 40 * * * * 50 * * * * 60 * * * * 70 *
 GCTAGCGCCGCCACCATGGCAAGTCGTTGGCTGCTGGACCTGAAGGCTGCCGCTATGAGTCCTCTAA
 CGATCGCGCGGTGGTACCGGTCAAGCACCGACGGACTGGGACTTCGACGGCATACTCAGAAGATT
 M A X F V A A W T L K A A A M S L L >
 80 * * * * 90 * * * * 100 * * * * 110 * * * * 120 * * * * 130 * * * * 140 *
 CCGAGGTGCAAACGTACGTTCTCTATCATCCCATCAGGCCCTCAAGGCCGAGATCGCCGAGAGACT
 GGCTCCAGCTTGCATGCAAGAGAGATAGTAGGGTAGTCGGGGAGTTCTGGCTAGCGCTCTGA
 T E V E T Y V L S I I P S G P L K A E I A Q R L >
 150 * * * * 160 * * * * 170 * * * * 180 * * * * 190 * * * * 200 * * * * 210 *
 TGAGGATTTTGAGGGAAAGAACAGATCTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATC
 ACTCCTACAAAAACGTCCTTCTGTGCTAGAACCTGGAGATCACCTAACGATTCTGGTTAG
 E D V F A G K N T D L E A L M E W L K T R P I >
 220 * * * * 230 * * * * 240 * * * * 250 * * * * 260 * * * * 270 * * * * 280 *
 CTGTCACCTCTGACTAAGGGAAATTAGGGTTGTTACGCTCACCGTGCCTAGTGAGCGAGGACTGC
 GACAGTGGAGACTGATTCCTAAATCCAAACAAAGTGGAGTGGCACGGTCACTCGCTCTGACG
 L S P L T K G I L G F V F T L T V P S E R G L >
 290 * * * * 300 * * * * 310 * * * * 320 * * * * 330 * * * * 340 * * * * 350 *
 AGCGTAGACGATTGTCCTAAATGCGCTTAAATGGAAATGGAGACCCAAACACATGGACAGGGCAGTTAA
 TCGCATCTGCTAACAGGTTTACGGGATTACCTTACCTCTGGTTGTTGACCTGTCCCGTCATT
 Q R R R F V Q N A L N G N G D P N N M D R A V K >
 360 * * * * 370 * * * * 380 * * * * 390 * * * * 400 * * * * 410 * * * * 420 *
 ACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCAAAGGAAGTTGCACTCAGTTACTCACT
 TGATATGTTCTCGACTCTCCCTTACTGTAAGTACCTGTTCTCAACGTGAGTCATGAGTTGA
 L Y K K L K R E M T F H G A K E V A L S Y S T >
 430 * * * * 440 * * * * 450 * * * * 460 * * * * 470 * * * * 480 * * * * 490 *
 GGTGGCCTTGCCTAGTTGCACTGGGCTCATATACAACGGATGGGAACAGTGGACCAACAGAAGTGGCTCTTG
 CCACCGAACGGTCACGTACCCAGTATATGTTGGCTTACCTCTGCACTGGTGTCTCACCGAGAAC
 G A L A . S C M G L I Y N R M G T V T T E V A L >
 500 * * * * 510 * * * * 520 * * * * 530 * * * * 540 * * * * 550 * * * * 560 *
 GCCTAGTATGTCCTGGACTGGGATGCCCACATCGGTCCCAAGGGCAGATGGGACTAC
 CGGATCATACACGGTGAACACTCGTCAACGACTACGGGTTGAGCCAGGGTGTCCGTACCGCTGATG
 G L V C A T C E Q I A D A Q H R S H R Q M A T T >
 570 * * * * 580 * * * * 590 * * * * 600 * * * * 610 * * * * 620 * * * * 630 *
 CACCAACCCACTAAATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAACGGCATGGGACAA
 GTGGTTGGTGATTAGTCCTGACTCTGTCTAACATGATCGTCGTATGCCGATTCCGGTACCTCGTT
 T N P L I R E E N R M V L A S T T A K A M E Q >
 640 * * * * 650 * * * * 660 * * * * 670 * * * * 680 * * * * 690 * * * * 700 *
 ATGGCTGGATCAAGTGGAGCAGGCGAGGGCATGGAAAGTCGCAAGTCAGGCTAGACAAATGGTGCAGG
 TACCGACCTAGTTACTCGTCCGTCGTCTCCGGTACCTCAGCGTTCAGTCCGATCTGTTACACGTC
 M A G S S E Q A A E A M E V A S Q A R Q M V Q >

FIGURE 7

710 720 730 740 750 760 770
* * * * * * *
CAATGAGGACAATTGGGACTCACCTAGCTCCAGTGCAGGTCTAAAGATGATCTTATTGAAAATTGCA
GTTACTCCTGTTAACCTGAGTGGGATCGAGGTACGTCCAGATTTCTACTAGAATAACTTTAACGT
A M R T I G T H P S S S A G L K D D L I E N L Q>
780 790 800 810
* * * * * * *
GGCTTACCAAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAGTGA
CCGAATGGTCTTGCTACCCCCACGTCTACGTCGCTAAGTTCACT
A Y Q K R M G V Q M Q R F K * >

FIGURE 7 CONTINUED

10 20 30 40 50 60 70

* * * * * * *

GCTAGCGCCGCCACCATGGCCAAGTTCGTGGCTGCCCTGGACCCCTGAAGGCTGCCGTCTCGAGATTGGGG
CGATCGCGCGGTGGTACCGGTTCAAGCACCACGGACCTGGACTTCGACGGCAGAGCTCTAACCCC
M A K F V A A W T L K A A A L E I G>

80 90 100 110 120 130 140

* * * * * * *

GACCCCTGCCTGAACGCCGAGAACATCACATCAGGATTCTAGGACCCCTCTCGTGTACAGGGGGGTT
CTGGGACGGACTTGGCTCTTGAGTAGCTAAGGATCTGGGAAGAGCACAATGTCCGCCCCAA
G P C L N A E N I T S G F L G P L L V L Q A G F>

150 160 170 180 190 200 210

* * * * * * *

TTTCTTGTGACAAGAACATCCTACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTCTA
AAAGAACAACTGTTCTAGGAGTTATGGCGTCTCAGATCTGAGCACCACTGAAGAGAGTTAAAGAT
F L L T R I L T I P Q S L D S W W T S L N F L>

220 230 240 250 260 270 280

* * * * * * *

GGGGAACTACCGTGTCTGGCCAAAATCGCAGTCCCCAACCTCCAATCACTCACCAACCTCTGTC
CCCCCTTGATGGCACACAGAACCGTTTAAGCGTCAGGGTTGGAGGTTAGTGAGTGGTGGAGAACAG
G G T T V C L G Q N S Q S P T S N H S P T S C>

290 300 310 320 330 340 350

* * * * * * *

CTCCAACCTTGTCTGGTTATCGCTGGATGTTCTGGCTGGTTATCATCTTCTCTCATCTGCTGCT
GAGGTTGAAAGGACCAATAGCGACCTACACAGACGCCAATAAGTAGAAGGAGAAAGTAGGACGACGA
P P T C P G Y R W M C L R R F I I F L F I L L L>

360 370 380 390 400 410 420

* * * * * * *

ATGCCCTCATCTTCTTGTGGTTCTCTGGACTATCAAGGTATGTTGCCGTTTGTCTCTAATTCCAGGA
TACGGAGTAGAAGAACCAACCAAGAACCTGATAGTTCCATACAACGGCAAACAGGAGATTAGGTCT
C L I F L L V L L D Y Q G M L P V C P L I P G>

430 440 450 460 470 480 490

* * * * * * *

TCCCTCAACAAACCGACGGGACCATGCCGACCTGCATGACTACTGCTCAAGGAACCTCTATGTATCCCT
AGGAGTTGGTGGTGGCTGCGCTGGTACGGCTGGACTGATGACGAGTTCTGGAGATACTAGGGAA
S S T T S T G P C R T C M T T A Q G T S M Y P>

500 510 520 530 540 550 560

* * * * * * *

CCTGTTGCTGTACCAAAACCTCGGACGGAAATTGACCGTATTCCCATCCCACATCCTGGGCTTTCGG
GGACAAACGACATGGTTGGARGCCTGCCTTAACGTGGACATAAGGGTAGGGTAGTAGGACCCGAAAGCC
S C C C T K P S D G N C T C I P I P S S W A F G>

570 580 590 600 610 620 630

* * * * * * *

AAAATTCTATGGGAGTGGGCCTCAGGCCGTTCTCTGGCTCAGTTACTAGTGCCTTGTTCAGTGG
TTTAAAGGATACCTCACCCGGAGTCGGGAAAGAGGACCGAGTCATACTGATCACGGTAAACAAGTCACC
K F L W E W A S A R F S W L S L L V P F V Q W>

FIGURE 8

640 650 660 670 680 690 700
*
TTCGTAGGGCTTCCCCCACTGTTGGCTTCAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGT
AAGCATCCGAAAGGGGGTGACAAACCGAAAGTCAATATAACCTACTACACCATAACCCCCGGTTCAGACA
F V G L S P T V W L S V I W M M W Y W G P S L >
710 720 730 740 750 760 770
*
ACAGCATCTTGAGTCCCTTTTACCGCTGTTACCAATTTCCTTTGTCTTTGGGTATACATTTAACCCCT
TGTCGTAGAACTCAGGGAAAAATGGCGACAATGGTTAAAGAAAACAGAAACCCATATGTAATTGGGA
Y S I L S P F L P L L P I F F C L W V Y I * >
780 790 800
*
AACAAAACAAAGAGATGGGGTTACTCTCTAA
TTGTTTGTCTCTACCCAAATGAGAGATT

FIGURE 8 CONTINUED

10 20 30 40 50 60 70
 GCTAGCGCCGCCACCATGCCAGGGGTCTAGAAGCCCTCAGAGCCCCCTGCCCTCTCCCTCTCTCTCAT
 CGATCGGGCGGTGCTACGGTCCCCAGATCTCGGGAGTCTCGGAGCGAGGAGGAAGAAAGCTA
 M P C G L E A L R A L P L L F L S >

80 90 100 110 120 130 140
 AGCCCTGTTCCCGATGCCAGGCCATGCCAGGCCCTGTCACGCCAGGAAATCAACGA
 TCGGGACAAACCCAGGGCTACGGTCCCGTAGTCGGTCCGACACGTGCGGCAGTGGCTTTAGTTGCT
 Y A C L G P G C Q A I S Q A V H A A H A E I N E >

150 160 170 180 190 200 210
 AGCTCGGAAGAACCCCTCCAGCTTATGCCCTCCAAACGCCCTCTATCCCTGTTCTTCTGCTGACCAAAATC
 TCGACCTTCTTGGGGAGGTGAAATAGCGGGAGGTTTGGAGGATAAGAACAGGACTGGCTTTRG
 A G R T P P A Y R P P N A P I L F F L L T R I >

220 230 240 250 260 270 280
 CTGACAATCCCCCAGTCCCTGCCAGGCCAAGTTGGTGGCTGCCCTGAAAGCTGCCCTGGATCA
 CACTGTTAGGGGCTGCCAGGACTGGGTTCAACGCCAGGACTGGGACTTCCGACGGGACCCCTAGT
 L T I P Q S L D A K F V A A W T L K A A A G I >

290 300 310 320 330 340 350
 TCTTGCTGTTCTGCACTGGTGGCCAGGGACGGCTGGCTATTCAAGAAACGGTGGAAAATGAGAAAGTT
 AGAACGACAAGACACGTCAACCGTCCCTGGGACGACGATAAGTCCTTGCACCGTTTACTCTCAA
 I L L F C A V V P G T L L F R K R W Q N E K F >

360 370 380 390 400 410 420
 TGGGCTGGACATGCCAGATGACTATGAAGATGAAATCTCTATGAGGGGCTGAAACCTTGATGACTGTTCT
 ACCCCACCTGTACGGTCTACTGATACTCTACTTTAGAGATACTCCGGACTTCCAACACTGACAAGA
 G V D M P D D Y E D E N L Y E G L N L D D C S >

430 440 450 460 470 480 490
 ATGTATGAGGACATCTCCAGGGGACTCCACGGCACCTACCAAGGATGIGGGCAACCTCCACATTGGAGATG
 TACATACTCTGTAGAGCTCCCTGAGGTCCCCTGAGATGGTCTACACCCGTGGAGGTGTAACCTCTAC
 M Y E D I S R G L Q G T Y Q D V G N L H I G D >

500 510
 CCCAGCTGGAAAAGCCATGAGGTACC
 GGGTGGACCTTTCGGTACTCCATGG
 A Q L E K P >

FIGURE 9

10 20 30 40 50 60 70
 * * * * * * *
 GCTACCGCCGCCACCATGGCACACTGGTGTGCTTCATGCCCTGCCACTGGCTGTTGTCCTGCTGC
 CGATCGCGCGGTGGTACCGGTGACCACGACAGAAGGTACGGGACGGTGACCGACAACAAGGACGACG
 M A T L V L S S M P C H W L L F L >
 80 90 100 110 120 130 140
 * * * * * * *
 TGCTCTCTCAGGTGACCCGATGCCAGGCTGTGCACGGCCCTCACGCCGAAATCAACGAAGCTGGAAG
 ACGAGAAGAGTCCACTGGCTAGTOGGTCCGACACGTGCCGAGTCCGGCTTAGTTCGCTTCGACCTTC
 L L F S G E P I S Q A V H A A H A E I N E A G R >
 150 160 170 180 190 200 210
 * * * * * * *
 AACCCCTCCAGCTTATGCCCTCCAAACGCTCCATCCCTGTTCTGCTGACCAAGAACGACTGGTCTTAGGACTGTTAG
 TTGGGGAGGTGAAATAGCGGGAGGTTCGGAGGATAAGAACAGAACGACTGGTCTTAGGACTGTTAG
 T P P A Y R P P N A P I L F F L L T R I L T I >
 220 230 240 250 260 270 280
 * * * * * * *
 CCCCCAGTCCCCTGGACCCAGTTGGCTGCCCTGACGGCTGGCTATTATCTTGATCCAGA
 GGGTCAGGGACCTGCCCTCAAGCACCGACGGACTGGGACTCCGACGGGATAATAGAACTAGGTCT
 P Q S L D A K F V A A W T L K A A A I I L I Q >
 290 300 310 320 330 340 350
 * * * * * * *
 CCCTCTCATCATCCTCTCATCATGGCCCATCTCTGCTACTTGACAAAGGATGACGGCAAGGCTGG
 GGGAGGAGTAGTGGAGAAAGTAGTAACACGGCTACAGGACGATGAACCTGGCTACTGCCGTTCCGACC
 T L L I I L F I I V P I F L L L D K D D G K A G >
 360 370 380 390 400 410 420
 * * * * * * *
 GATGGAGGAAGATCACACCTATGAGGGCTTGAAACATTGACCAAGACAGCCACCTATGAAAGACATACTGACT
 CTACCTCTCTAGTGTGGATACTCCGAACCTGTAACTGGCTGTGGGATACTCTGTATCACTGAA
 M E E D H T Y E G L N I D Q T A T Y E D I V T >
 430 440 450 460 470 480
 * * * * * * *
 CTTCGGACAGGGGAGGTAAAGTGGTGGTAGGAGAGCATCCAGGCCAGGANTGAGGTAC
 GAAGCCCTGTCCTCCATTTCACCAAGCCATCTCGTAGGTCCGGCTTACTCCATGG
 L R T G E V K W S V G E H P G Q E >

FIGURE 10

10 20 30 40 50 60 70
* * * * * * *
GCTAGCCGCCACCATCGGAATCCACGGTGCAGATCAGAGCCCTGTTCTCCCTCCCTGTGGGTGCCCG
CGATCGCCGGGGTGGTACCCCTAACGTCCACGTCTAGGTCTCCGACAAAGACGAGGAGGACACCCACGGGC
M G M Q V Q I Q S L F L L L W V P>

80 90 100 110 120 130 140
* * * * * * *
GGTCCCAGGAATCACCCAGGCTGTCCACGGCCGTCACCCCGAAATCAACGAAGCTGGAAGAACCCCTCC
CCAGGGCTCCCTACTCGGTCCGACAGTGCCGGAGTGCCGTTACTTGCTTCGACCTTCGGGAGG
G S R G I S Q A V H A A H A E I N E A G R T P P>

150 160 170 180 190 200 210
* * * * * * *
AGCTTATCGCCCTCCAAAACGCTCTATCCCTGTTCTTGCTGACCAATCCCCCATGCC
TCGAATAGCGGGAGGCTTGGCAGGATAGGACAAGAAGACGACTGGCTTAGGACTGTTAGGGGGTCAGG
A Y R P P N A P I L F F L L T R I L T I P Q S>

220 230 240 250 260
* * * * *
CTGGACGCCAAGTTCGTGGCTGGCACCCCTGAAGGCTGCCGTTGAGGTACC
GACCTGGGTTCAAGCACCGACGGACCTGGACTTCCGACGGCAACTCCATGG
L D A K F V A A W T L K A A A >

FIGURE 11

TTCCCG AGT CAC AGG AGG AGA AGC AGG AGC TGT CGG GAA GAT CAG AAG Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys	49
1 5 10	
CCA GTC ATG GAT GAC CAG CGC GAC CTT ATC TCC AAC AAT GAG CAA CTG Pro Val Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu	97
15 20 25 30	
CCC ATG CTG GGC CGG CGC CCT GGG GCC CCG GAG AGC AAG TGC AGC CGC Pro Met Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg	145
35 40 45	
GGA GCC CTG TAC ACA GGC TTT TCC ATC CTG GTG ACT CTG CTC CTC GCT Gly Ala Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Ala	193
50 55 60	
GGC CAG GCC ACC ACC GCC TAC TTC CTG TAC CAG CAG CAG GGC CGG CTG Gly Gln Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gly Arg Leu	241
65 70 75	
GAC AAA CTG ACA GTC ACC TCC CAG AAC CTG CAG CTG GAG AAC CTG CGC Asp Lys Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg	289
80 85 90	
ATG AAG CTT CCC AAG CCT CCC AAG CCT GTG AGC AAG ATG CGC ATG GCC Met Lys Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala	337
95 100 105 110	
ACC CCG CTG CTG ATG CAG GCG CTG CCC ATG GGA GCC CTG CCC CAG GGG Thr Pro Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly	385
115 120 125	
CCC ATG CAG AAT GCC ACC AAG TAT GGC AAC ATG ACA GAG GAC CAT GTG Pro Met Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val	433
130 135 140	
ATG CAC CTG CTC CAG AAT GCT GAC CCC CTG AAG GTG TAC CCG CCA CTG Met His Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu	481
145 150 155	
AAG GGG AGC TTC CCG GAG AAC CTG AGA CAC CTT AAG AAC ACC ATG GAG Lys Gly Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu	529
160 165 170	
ACC ATA GAC TGG AAG GTC TTT GAG AGC TGG ATG CAC CAT TGG CTC CTG Thr Ile Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu	577
175 180 185 190	

FIGURE 12

FIGURE 12 Continued

CCGCCTCGGC ATG GCG CCC CGC AGC GCC CGG CGA CCC CTG CTG CTG CTA Met Ala Pro Arg Ser Ala Arg Arg Pro Leu Leu Leu	229
1 5 10	
CTG CCT GTT GCT GCT CGG CCT CAT GCA TTG TCG TCA GCA GCC ATG Leu Pro Val Ala Ala Ala Arg Pro His Ala Leu Ser Ser Ala Ala Met	277
15 20 25	
TTT ATG GTG AAA AAT GGC AAC GGG ACC GCG TGC ATA ATG GCC AAC TTC Phe Met Val Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe	325
30 35 40 45	
TCT GCT GCC TTC TCA GTG AAC TAC GAC ACC AAG ACT GGC CCC AAG AAC Ser Ala Ala Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn	373
50 55 60	
ATG ACC TTT GAC CTG CCA TCA GAT GCC ACA GTG GTG CTC AAC CGC AGC Met Thr Phe Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser	421
65 70 75	
TCC TGT GGA AAA GAG AAC ACT TCT GAC CCC AGT CTC GTG ATT GCT TTT Ser Cys Gly Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe	469
80 85 90	
GGA AGA GGA CAT ACA CTC ACT CTC AAT TTC ACG AGA AAT GCA ACA CGT Gly Arg Gly His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg	517
95 100 105	
TAC AGC GTT CAG CTC ATG AGT TTT GTT TAT AAC TTG TCA GAC ACA CAC Tyr Ser Val Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His	565
110 115 120 125	
CTT TTC CCC AAT GCG AGC TCC AAA GAA ATC AAG ACT GTG GAA TCT ATA Leu Phe Pro Asn Ala Ser Ser Lys Glu Ile Lys Thr Val Glu Ser Ile	613
130 135 140	
ACT GAC ATC AGG GCA GAT ATA GAT AAA AAA TAC AGA TGT GTT AGT GGC Thr Asp Ile Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly	661
145 150 155	
ACC CAG GTC CAC ATG AAC AAC GTG ACC GTA ACG CTC CAT GAT GCC ACC Thr Gln Val His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr	709
160 165 170	
ATC CAG GCG TAC CTT TCC AAC AGC AGC TTC AGC AGG GGA GAG ACA CGC Ile Gln Ala Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg	757
175 180 185	

FIGURE 13

TGT GAA CAA GAC AGG CCT TCC CCA ACC ACA GCG CCC CCT GCG CCA CCC Cys Glu Gln Asp Arg Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro 190 195 200 205	805
AGC CCC TCG CCC TCA CCC GTG CCC AAG AGC CCC TCT GTG GAC AAG TAC Ser Pro Ser Pro Val Pro Lys Ser Pro Ser Val Asp Lys Tyr 210 215 220	853
AAC GTG AGC GGC ACC AAC GGG ACC TGC CTG CTG GCC AGC ATG GGG CTG Asn Val Ser Gly Thr Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu 225 230 235	901
CAG CTG AAC CTC ACC TAT GAG AGG AAG GAC AAC ACG ACG GTG ACA AGG Gln Leu Asn Leu Thr Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg 240 245 250	949
CTT CTC AAC ATC AAC CCC AAC AAG ACC TCG GCC AGC GGG AGC TGC GGC Leu Leu Asn Ile Asn Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly 255 260 265	997
GCC CAC CTG GTG ACT CTG GAG CTG CAC AGC GAG GGC ACC ACC GTC CTG Ala His Leu Val Thr Leu Glu Leu His Ser Glu Gly Thr Thr Val Leu 270 275 280 285	1045
CTC TTC CAG TTC GGG ATG AAT GCA AGT TCT AGC CGG TTT TTC CTA CAA Leu Phe Gln Phe Gly Met Asn Ala Ser Ser Arg Phe Phe Leu Gln 290 295 300	1093
GGA ATC CAG TTG AAT ACA ATT CTT CCT GAC GCC AGA GAC CCT GCC TTT Gly Ile Gln Leu Asn Thr Ile Leu Pro Asp Ala Arg Asp Pro Ala Phe 305 310 315	1141
AAA GCT GCC AAC GGC TCC CTG CGA GCG CTG CAG GCC ACA GTC GGC AAT Lys Ala Ala Asn Gly Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn 320 325 330	1189
TCC TAC AAG TGC AAC GCG GAG GAG CAC GTC CGT GTC ACG AAG GCG TTT Ser Tyr Lys Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe 335 340 345	1237
TCA GTC AAT ATA TTC AAA GTG TGG GTC CAG GCT TTC AAG GTG GAA GGT Ser Val Asn Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly 350 355 360 365	1285
GGC CAG TTT GGC TCT GTG GAG GAG TGT CTG GAC GAG AAC AGC ACG Gly Gln Phe Gly Ser Val Glu Glu Cys Leu Leu Asp Glu Asn Ser Thr 370 375 380	1333

FIGURE 13. CONTINUED

CTG ATC CCC ATC GCT GTG GGT GCC CTG GCG GGG CTG GTC CTC ATC Leu Ile Pro Ile Ala Val Gly Gly Ala Leu Ala Gly Leu Val Leu Ile 385 390 395	1381
GTC CTC ATC GCC TAC CTC GTC GGC AGG AAG AGG AGT CAC GCA GGC TAC Val Leu Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser His Ala Gly Tyr 400 405 410	1429
CAG ACT ATC TAGCCTGGTG CACGCAGGCA CAGCAGCTGC AGGGGCCTCT Gln Thr Ile 415	1478

FIGURE 13 CONTINUED

10 20 30 40 50 60 70
 * * * * * * * * *
 ATGATCACATTCTGCCGCTGCTGGGGCTCAGCCTGGGCTGCACAGGAGCAGGTGGCTTCGTGGCCC
 TACTAGTGTAAAGGACGGCGACGACGACCCGAGTCGGACCCGACGTGTCCTCGTCCACCGAAGCACCGGG
 M I T F L P L L G L S L G C T G A G G F V A >
 80 90 100 110 120 130 140
 * * * * * * * * * *
 ATGGAAAGCACCTGTCGGATGATGCTGGACTCAAAGGATTCACATACTGCATCTCCCAA
 TACACCTTCGTCGGACAGAACCTACTACGACCCGAGGTTCTAAAGTGTATGACGTAGAGGAAGTT
 H V E S T C L L D D A G T P K D F T Y C I S F N >
 150 160 170 180 190 200 210
 * * * * * * * * * *
 CAAGGATCTGCTGACCTGCTGGATCCAGAGGAGATAAGATGGCCCTTGCGAATTGGGGTGTGAAT
 GTTCTAGACGACTGGACGACCCTAGGTCTCCTCTTATTCTACCGGGAACGCTTAAACCCCAAGCTTA
 K D L L T C W D P E E N K M A P C E F G V L N >
 220 230 240 250 260 270 280
 * * * * * * * * * *
 AGCTGGCGAATGTCCTCTCACAGCACCTCAACCAAAAAAGACACCCCTGATGCGAGCGCTTGCGCAATGGC
 TCGAACCGCTTACAGGAGAGTCGTGGAGTTCTGTGGGACTACGTCGCGAAGGCGTTACCCG
 S L A N V L S Q H L N Q K D T L M Q R L R N G >
 290 300 310 320 330 340 350
 * * * * * * * * * *
 TTCTAGAATTGTGCCACACACACCCAGCCCTCTGGGGATCACTGACCAACAGGACACGGCACCGACCACATCTGT
 AAGTCTTAACACGGTGTGTGGTGGGAAGACCCCTAGTGACTGGTTGTCCTGTGCCGTGGTAGACA
 L Q N C A T E T Q P F W G S L T N R T R P P S V >
 360 370 380 390 400 410 420
 * * * * * * * * * *
 GCAAGTAGCCAAAACCACTCTTTAACACGAGGGAGCCCTGTGATGCTGGCTGCTATGTGTGGGGCTTC
 CGTCATGGTTGGTGGAAAATTGTGCTCCCTCGGACACTACGACCGACGATAACACACCCCGAAG
 Q V A K T T P F N T R E P V M L A C Y V W G F >
 430 440 450 460 470 480 490
 * * * * * * * * * *
 TATCCAGCAGAAGTGAATCACGTGGAGGAAGAACGGGAAGCTTGTATGCCCTCACAGCAGTGGCGACA
 ATAGGTGCTTCACTGATAGTGCACCTCCCTTGCCCTCGAACAGTACGGAGTGTGTCACGCGTGT
 Y P A E V T I T W R K N G K L V M P H S S A H >
 500 510 520 530 540 550 560
 * * * * * * * * * *
 AGACTGCCAGCCCAATGGAGACTGGACATACCAAGACCCCTCTCCATTAGCCTTAACCCCTCTTACGG
 TCTGACGGGTGGTTACCTCTGACCTGTATGGTCTGGGAGAGGGTAAATCGGAATTGGGGAGAACGCC
 K T A Q P N G D W T Y Q T L S H L A L T P S Y G >

FIGURE 14

570 580 590 600 610 620 630

* * * * * * *

GGACACTTACACCTGTGTGGTAGAGCACATTGGGGCTCCTGAGCCATCCCTCGGGACTGGACACCTGG
CCTGTGAATGTGGACACACCATCTCGTGAACCCGAGGACTCGGGTAGGAAGCCCTGACCTGTGGACCC
D T Y T C V V E H I G A P E P I L R D W T P G >

640 650 660 670 680 690 700

* * * * * * *

CTGTCCCCCATGCAGACCCCTGAAGGTTCTGTGTCTGCAGTGACTCTGGGCCTGGGCCTCATCATCTTCT
GACAGGGGGTACGTCTGGACTTCAAAGACACAGACGTCACTGAGACCCGGACCCGGAGTAGTAGAAGA
L S P M Q T L K V S V S A V T L G L G L I I F >

710 720 730 740 750 760 770

* * * * * * *

CTCTGGTGTGATCAGCTGGGGAGAGCTGGCCACTCTAGTTACACTCCTCTGGGTCCAATTATTC
GAGAACCAACTAGTCGACCCCTCTGACCCGGTGAAGATCAATGTGAGGAGAAGGACCCAGGTTAATAAG
S L G V I S W R R A G H S S Y T P L P G S N Y S >

780 790

* * *

AGAAGGATGGCACATTCTAG
TCTTCCTACCGTGTAAAGGATC
E G W H I S * >

FIGURE 14 Continued

10 20 30 40 50 60 70
 * * * * * * *
 ATGGGTTCTGGGTGGGTCCCCTGGGTGGCTCTGCTAGTGAATCTGACCCAACGGATTCCATGA
 TACCAAGACCCACCCAGGGGACCCACCAACCGAGACGATCACTTAGACTGGTTGACCTAAGGAGGTACT
 M G S G W V P W V V A L L V N L T Q L D S S M>
 80 90 100 110 120 130 140
 * * * * * * *
 CTCAAGGCACAGACTCTCCAGAAGATTGGTGAATCAGGAAAGGCTGACTGTTACTTCACCAACGGAC
 GAGTTCCCGTGTCTGAGAGGTCTCTAAAACACTAAGTCCGTTCCGACTGACAATGAAGTGGTTGCCCTG
 T Q G T D S P E D F V I Q A K A D C Y F T N G T>
 150 160 170 180 190 200 210
 * * * * * * *
 AGAAAAGGTGCAGTTGGTCAGATTCACTTTAACTTGGAGAGTATGTACGTTGACAGTGATGTG
 TCTTTCCACGTCAAACACCGTCAAGTAGAAATTGAACCTCCTCATACATGCAAAGCTGTCACTACAC
 E K V Q F V V R F I F N L E E Y V R F D S D V>
 220 230 240 250 260 270 280
 * * * * * * *
 GGGATGTTTGGCATGGCAAGCTGGGGCAGCCAGATGCTGAGCAGTGGAACAGCCGGCTGGATCTCT
 CCCTACAAACACCGTAACTGGTTCGACCCCGTCGGTCTACGACTCGTCACTTGTGGCCGACCTAGAGA
 G M F V A L T K L G Q P D A E Q W N S R L D L>
 290 300 310 320 330 340 350
 * * * * * * *
 TGGAGAGGAGCAGACAGGCCGTGGATGGGTCTGTAGACACAACACTACAGGCTGGCGCACCTTCACTGT
 ACCTCTCCTCGTCTGTCCGGCACCTACCCAGACATCTGTGTATGTCCGACCCCGTGGGAAGTGACA
 L E R S R Q A V D G V C R H N Y R L G A P F T V>
 360 370 380 390 400 410 420
 * * * * * * *
 GGGGAGAAAAGTGCACCCAGAGGTGACAGTGTACCCAGAGAGGGACCCACTCCTGCACCGATAATCTG
 CCCCTCTTTCACGTTGGCTCCACTGTACATGGGTCTCTCCTGGGTGAGGACGTGGTCGTATTAGAC
 G R K V Q P E V T V Y P E R T P L L H Q H N L>
 430 440 450 460 470 480 490
 * * * * * * *
 CTGCACTGCTCTGTGACAGGCTCTATCCAGGGGATATCAAGATCAAGTGGTCTGAATGGGCAGGAGG
 GACGTGACGAGACACTGTCCGAAGATAGGTCCCTATAGTTCTAGTTCACCAAGGACTTACCCGTCC
 L H C S V T G F Y P G D I K I K W F L N G Q E>
 500 510 520 530 540 550 560
 * * * * * * *

FIGURE 15

AGAGAGCTGGGTCACTGTCACGGCCATCAGGAATGGAGACTGGACCTTCAGACTGTGGTATGCT
 TCTCTGACCCAGTACAGGTGACCGGGATAGTCCTAACCTCTGACCTGAAAGTCTGACACCACTACGA
 E R A G V M S T G P I R N G D W T F Q T V V M L>
 *
 570 580 590 600 610 620 630
 AGAAAATGACTCCTGAACCTGGACATGTCTACACCTGCCTTGTGATCACTCCAGCCTGCTGAGCCCTGTT
 TCTTTACTGAGGACTTGAAACCTGTACAGATGTGGACGGAACAGCTAGTGAGGTGGACGACTCGGGACAA
 E M T P E L G H V Y T C L V D H S S L L S P V>
 *
 640 650 660 670 680 690 700
 TCTGTGGAGTGGAGAGCTCAGTCTGAATAATTCTGGAGAAAGATGCTGAGTGGCATTGCGAGCCTTCTAC
 AGACACCTCACCTCTCGAGTCAGACTTATAAGAACCTTTCTACGACTCACCGTAACGTCGGAAGGATG
 A Q S E Y S W R K M L S G I A A F L>
 S V E W R A Q S E Y S W R K M L S G I A A F L>
 *
 710 720 730 740 750 760 770
 TTGGGCTAATCTTCTTCTGGGGAAATCGTCATCCAGCTAAGGGCTCAGAAAGGATATGTGAGGACGCA
 AACCCGATTAGAAGGAAGACCACCCCTAGCAGTAGGTCGATTCCGAGTCTTCCTATAACACTCCTGCGT
 L G L I F L L V G I V I Q L R A Q K G Y V R T Q>
 *
 780 790 800 810 820
 GATGTCTGGTAATGAGGTCTCAAGAGCTGTTCTGCTCCCTCAGTCATGCTAA
 CTACAGACCATTACTCCAGAGTTCTCGACAAGACGAGGGAGTCAGTACGATT
 M S G N E V S R A V L L P Q S C *>

FIGURE 15 CONTINUED

10 20 30 40 50 60 70
 * * * * * * *
 ATGCCCTGGGGTCCAGGAGTCCTCCAAGCTCTGCCCTGCCACCATCTTCCCTCCTCTTGCTGTGCTG
 TACGGACCCCCAGGTCTCAGGAGGTTGAGACGGACGGTGGTAGAAGGAGAGAAGGACGACAGACGAC
 M P G G P G V L Q A L P A T I F L L F L L S A >
 80 90 100 110 120 130 140
 * * * * * * *
 TCTACCTGGGCCCTGGTGCAGGCCCTGTGGATGCACAAGGTCCCAGCATCATTGATGGTGAGCCTGGG
 AGATGGACCCGGGACCCACGGTCCGGGACACCTACGTGTTCCAGGGCGTAGTAACCTACACTCGGACCC
 V Y L G P G C Q A L W M H K V P A S L M V S L G >
 150 160 170 180 190 200 210
 * * * * * * *
 GGAAGACGCCCACTTCACTGCCGCACAATAGCAGCAACAAGCCAACGTACCTGGTGGCGCGTCCTC
 CCTCTGCGGGTGAAGGTTACGGCGTGTATCGTCGTTGCGGTTGCGATGGACCAACCGCGCAGGAG
 E D A H F Q C P H N S S N N A N V T W W R V L >
 220 230 240 250 260 270 280
 * * * * * * *
 CATGGCAACTACACGTGGCCCCCTGAGTTCTGGGCCCCGGCGAGGACCCCAATGGTACGCTGATCATCC
 GTACCGTTGATGTCACCAGGGACTCAAGAACCCGGCCCGCTCTGGGTTACCATGCGACTAGTAGG
 H G N Y T W P P E F L G P G E D P N G T L I I >
 290 300 310 320 330 340 350
 * * * * * * *
 AGAATGTGAACAAGAGCCATGGGGCATATACGTGTCGGGTCAGGAGGGCAACGAGTCATAACAGCA
 TCTTACACTTGTCTCGTACCCCGTATATGCACACGGCCAGGTCTCCGTTGCTCAGTATGGTCGT
 Q N V N K S H G G I Y V C R V Q E G N E S Y Q Q >
 360 370 380 390 400 410 420
 * * * * * * *
 GTCCTGCGGACCTACCTCCGGTGCAGCCAGCCGCCCTTCCTGGACATGGGGAGGGCACC
 CAGGACGCGTGGATGGAGGCGCACGCGGTGGGGGGTCCGGGAAGGACCTGTACCCCTCCCGTGG
 S C G T Y L R V R Q P P P R P F L D M G E G T >
 430 440 450 460 470 480 490
 * * * * * * *
 AAGAACCGAATCATCACAGCCGAGGGGATCATCCTCTGTTCTGCCGGTGGTGCCTGGACGCTGCTGC
 TTCTGGCTTAGTAGTGTGCGCTCCCTAGTAGGAGGACAAGACGCGCCACACGGACCCCTGCGACGACG
 K N R I I T A E G I I L L F C A V V P G T L L >

FIGURE 16

500	510	520	530	540	550	560
*	*	*	*	*	*	*
TGTCAGGAAACGATGGCAGAACGAGAAGCTCGGGTTGGATGCCGGGGATGAATATGAAGATGAAAACCT						
ACAAGTCCTTGTACCGTCTTGTGAGCCAACCTACGGCCCCACTTATACTTCTACTTTGGA						
L F R K R W Q N E K L G L D A G D E Y E D E N L >						
570	580	590	600	610	620	630
*	*	*	*	*	*	*
TTATGAAGGCCTGAACCTGGACGACTGCTCATGTATGAGGACATCTCCCGGGGCTCCAGGGCACCTAC						
AATACTTCCGGACTTGGACCTGCTGAGGATACACTCCTGTAGAGGGCCCCGGAGGTCCCCTGGATG						
Y E G L N L D D C S M Y E D I S R G L Q G T Y >						
640	650	660	670	680	690	700
*	*	*	*	*	*	*
CAGGATGTGGCAGCCTCAACATAGGAGATGTCCAGCTGGAGAAGCCGTGACACCCCTACTCCTGCCAGG						
GTCCTACACCCGTCGGAGTTGTATCCTCTACAGGTGACCTCTCGGCACGTGGGGATGAGGACGGTCC						
Q D V G S L N I G D V Q L E K P * >						

FIGURE 16 CONTINUED

GAATTCCGCG GTGACC ATG GCC AGG CTG GCG TTG TCT CCT GTG CCC AGC Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser 1 5 10	49
CAC TGG ATG GTG GCG TTG CTG CTG CTG CTC TCA GCT GAG CCA GTA CCA His Trp Met Val Ala Leu Leu Leu Leu Ser Ala Glu Pro Val Pro 15 20 25	97
GCA GCC AGA TCG GAG GAC CGG TAC CGG AAT CCC AAA GGT AGT GCT TGT Ala Ala Arg Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys 30 35 40	145
TCG CGG ATC TGG CAG AGC CCA CGT TTC ATA GCC AGG AAA CGG CGC TTC Ser Arg Ile Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Arg Phe 45 50 55	193
ACG GTG AAA ATG CAC TGC TAC ATG AAC AGC GCC TCC GGC AAT GTG AGC Thr Val Lys Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser 60 65 70	241
TGG CTC TGG AAG CAG GAG ATG GAC GAG AAT CCC CAG CAG CTG AAG CTG Trp Leu Trp Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu 80 85 90	289
GAA AAG GGC CGC ATG GAA GAG TCC CAG AAC GAA TCT CTC GCC ACC CTC Glu Lys Gly Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu 95 100 105	337
ACC ATC CAA GGC ATC CGG TTT GAG GAC AAT GGC ATC TAC TTC TGC CAG Thr Ile Gln Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln 110 115 120	385
CAG AAG TGC AAC AAC ACC TCG GAG GTC TAC CAG GGC TGC GGC ACA GAG Gln Lys Cys Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu 125 130 135	433
CTG CGA GTC ATG GGA TTC AGC ACC TTG GCA CAG CTG AAG CAG AGG AAC Leu Arg Val Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn 140 145 150 155	481
ACG CTG AAG GAT GGT ATC ATC ATG ATC CAG ACG CTG CTG ATC ATC CTC Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu 160 165 170	529

FIGURE 17

TTC ATC ATC GTG CCT ATC TTC CTG CTG CTG GAC AAG GAT GAC AGC AAG Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys 175 180 185	577
GCT GGC ATG GAG GAA GAT CAC ACC TAC GAG GGC CTG GAC ATT GAC CAG Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln 190 195 200	625
ACA GCC ACC TAT GAG GAC ATA GTG ACG CTG CGG ACA GGG GAA GTG AAG Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys 205 210 215	673
TGG TCT GTA GGT GAG CAC CCA GGC CAG GAG TGAGAGCCAG GTCGCCCAT Trp Ser Val Gly Glu His Pro Gly Gln Glu 220 225 230	723

FIGURE 17 CONTINUED

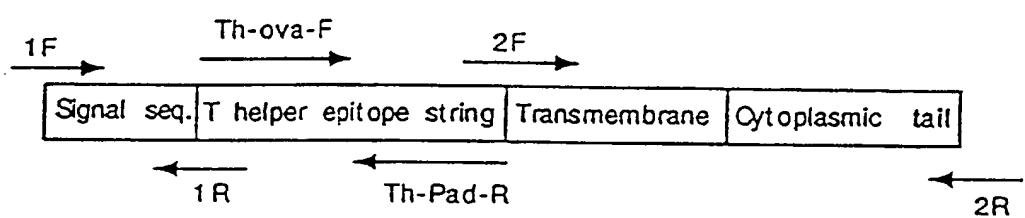


FIGURE 18

FIGURE 19

710 720 730 740 750 760 770
* * * * * * *
TGGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAAATGTCGTAAACAACCTCCGGCCCCATTGACG
ACCCTCAAACAAAACCGTGGTTAGTTGCCCTGAAAGGTTACAGCATTGTCGAGGGGGTAAGTC
780 790 800 810 820 830 840
* * * * * * *
CAAATGGGCGTAGGGCGTACGGTGGGAGGTCTATATAAGCAGCTCTGGCTAACTAGAGAACCCA
GTTTACCCGCATCCGCACATGCCACCCCTCCAGATATATTGCTCGAGAGACCGATTGATCTCTGGGT
850 860 870 880 890 900 910
* * * * * * *
CTGCTTACTGGCTTATCGAAATTAAACGACTCACTATAGGGAGACCCRAAGCTGGCTAGAGTAAGTACCG
GACGAATGACCGAATAGCTTAAATTATGCTGAGTGTATCCCTCTGGGTTGACCGATCTCATCGGC
920 930 940 950 960 970 980
* * * * * * *
CCTATAGAGTCTATAGGCCACCCCTGGCTTATGCATGCTATACTGTTTTGGCTGGGTCTAT
GGATATCTCAGATATCGGGTGGGGAACCGAAGAACGATACGTACGATATGACAAAAACCGAACCCAGATA
990 1000 1010 1020 1030 1040 1050
* * * * * * *
ACACCCCCGTTCTCATGTTATAGGTGATGGTATAGCTTAGGCTATAGGTGTTGGTTATTGACCAATT
TGTGGGGCGAAGGAGTACAATATCCACTACCATATCGAATCGGATATCCACACCCATAACTGGTAATA
1060 1070 1080 1090 1100 1110 1120
* * * * * * *
TGACCACTCCCCATTGGTGACGATACTTCCATTACTAACATGGCTTTGCCACAACTCTC
ACTGGTGAGGGATAACCAACTGCTATGAAAGTAATGATTAGGTATTGTACCGAGAACGGTGTGAGAG
1130 1140 1150 1160 1170 1180 1190
* * * * * * *
TTTATTGGCTATGCCAATACACTGTCCTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGG
AAATAACCGATATACGGTTATGTGACAGGAAGTCTCTGACTGTGCTGAGACATAAAATGTCCTACCC
1200 1210 1220 1230 1240 1250 1260
* * * * * * *
TCTCATTATTATTTACAAATTACACATATACACACCCACCGTCCCCAGTGGCCCGAGTTTTATTAACAA
AGAGTAATAATAAAATGTTAGTGATATGTTGGTGGCAGGGGTACGGCGTAAAAATAATTG
1270 1280 1290 1300 1310 1320 1330
* * * * * * *
TAACGTGGGATCTCACCGGAATCTGGGTACGTGTTCCGGACATGGGCTTCTCCGGTAGGGGGAG
ATTGACCCCTAGAGGTGCGCTTAGAGCCCATGACAAGGCGTACCCGAGAAGAGGCCATCGCCGCTC
1340 1350 1360 1370 1380 1390 1400
* * * * * * *
CTTCTACATCCGAGCCCTGCTCCATGCCCTCAGCGACTCATGGTCGCTCGGAGCTCTGCTCTAAC
GAAGATGTAAGGCTGGGAGGGTACGGAGGTGAGTACCGAGCGAGGCCGTCGAGGAACGAGGATTG

FIGURE 19 CONTINUED

1410 1420 1430 1440 1450 1460 1470
 * * * * * * *
 AGTGGAGGCCAGACTTAGGCACGACAGATGCCACCACCACTGTGCCGACAAGGCCGTGGCGTA
 TCACCTCCGGTCTGAATCCGTGCTGCTACGGTGGTGGTCACACGGCGTTCGGCACCGCCAT
 1480 1490 1500 1510 1520 1530 1540
 * * * * * * *
 GGGTATGTGTCAGAAAATGAGCTGGGGAGCGGGCTTGACCGCTGACGCATTGAAAGACTAAGGCAG
 CCCATACACAGACTTTACTCGAGCCCTCGCCCGAACGTGGCAGTCGTAAACCTCTGAATTCCGTC
 1550 1560 1570 1580 1590 1600 1610
 * * * * * * *
 CGGCAGAAGAAGATGCAGGCAGCTGAGTTGTGTTCTGATAAGAGTCAGAGGTAACCTCCGTTGGCGT
 GCCGTCCTCTTCTACGTCCGTCAGTCACACACACAGACTATTCTCAGTCCTCATTGAGGGCAACGCCA
 1620 1630 1640 1650 1660 1670 1680
 * * * * * * *
 GCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAGACATAAT
 CGACAATTGCCACCTCCCGTACATCAGACTCGTCAGTCAGCAACGACGGCGCGCGCGGTGGTCTGTATTA
 1690 1700 1710 1720 1730 1740 1750
 * * * * * * *
 AGCTGACAGACTAACAGACTGTTCTTTCATGGCTTTCTGAGGCTAGCCGGCTGAATTGGATA
 TCGACTGTCGATTGTCGACAGGAAAGGTACCCAGAAAAGACGTCCGATCGGGGACTTAAGCCTAT
 1760 1770 1780 1790 1800 1810 1820
 * * * * * * *
 TCCAAGCTTGATGAATAAAAGATCAGAGCTCTAGTGATCTGTGTTGGTTTTTGTGTCGAGCCCC
 AGGTTGAAACTACTTATTCTAGTCTCGAGATCACTAGACACACACACACAGAGCTCGGG
 1830 1840 1850 1860 1870 1880 1890
 * * * * * * *
 AGCTGGTTCTTCCGCCTCAGAAGCCATAGAGCCCACCGCATCCCCAGCATGCCCTGCTATTGTCCTCCCA
 TCGACCAAGAAGCGGAGTCTCGGTATCTGGTGGCGTAGGGTCGACGGACGATAACAGAAGGGT
 1900 1910 1920 1930 1940 1950 1960
 * * * * * * *
 ATCCCTCCCTTGCTGCTGCTGCCACCCACCCCCAGAAATAGAATGACACCTACTCAGACAATGCGAT
 TAGGAGGGGGAACGACAGGACGGGTGGGGTGGGGTCTTATCTTACTGTGGATGAGTCGTTACGCTA
 1970 1980 1990 2000 2010 2020 2030
 * * * * * * *
 GCAATTTCCTCATTATTAGGAAAGGACAGTGGGACTGGCACCTCCAGGGTCAAGGAAGGCACGGGG
 CGTTAAAGGAGTAAATAATCCTTCTGTCACCCCTACCGTGGAAAGGTCCAGTTCCGTGCCCC
 2040 2050 2060 2070 2080 2090 2100
 * * * * * * *
 AGGGCAAACAAACAGATGGCTGGCAACTAGAAGGCACAGTCGAGGCTGATCAGCGAGCTCTAGCGGTACC
 TCCCCGTTGTTGTCACCGACCGTTGATCTCCGTGTCAGCTCCGACTAGTCGCTCGAGATCGCCATGG

FIGURE 19 CONTINUED

2110 2120 2130 2140 2150 2160 2170
 * * * * * * *
 GGCATTAGTCTATGGCCGACTCTAGATTTCTCCTGGCGCCGCCCTAGATGCTGATCGACCTGC
 CCGTAATCAGATAACCGGCTGAGATCTAAAGAGGAACGCCGGGATCTACGTACGAGCTAGCTGGACG

 2180 2190 2200 2210 2220 2230 2240
 * * * * * * *
 AGTTGGACCTGGGAGTGGACACCTGTGGAGAGAAGGCAAGTGGATGTCAATTGTCACTCAAGTGTATGG
 TCAACCTGGACCCCTCACCTGTGGACACCTCTCTTCGTTACCTACAGTAACAGTGAGTTACATACC

 2250 2260 2270 2280 2290 2300 2310
 * * * * * * *
 CCAGATCTCAAGCTGCCACACCTCAAGCTAGCTTGTGACAACAAAAAGATTGTCTTCTGACCAGATGGA
 GGTCTAGAGTTCGGACGGTGTGGAGTTCGATCGACTGTGTCTAACAGAAAAGACTGGTCTACCT

 2320 2330 2340 2350 2360 2370 2380
 * * * * * * *
 CGCGGCCACCCCTCAAAGGCATACCGCGGGCCAGGTGAATATCAAATCCTCTCGTTTGGAAACTGAC
 GCGCCGGTGGGAGTTCCGTAGTGGCGCCGGTCCACTTATAGTTAGGAGGAGCAAAACCTTGACTION

 2390 2400 2410 2420 2430 2440 2450
 * * * * * * *
 AATCTTAGCGCAGAAGTCATGCCGTTTGGAGAGGGAGTACTCACCCCAACAGCTGGCCCTCGCAGACA
 TTAGAATCGCGTCTCAGTACGGCGAAAATCTCCCTCATGAGTGGGTTGTCGACCGGGAGCGTCTGT

 2460 2470 2480 2490 2500 2510 2520
 * * * * * * *
 GCGAATTAAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGCAAGCTAGCTGGGCTCCC
 CGCTTAATTAAAGGTCGTGTGACCGCCGGCAATGATCACCTAGGCTCGAGCGTTCGATCGAACCCAGAGGG

 2530 2540 2550 2560 2570 2580 2590
 * * * * * * *
 TATAGTGAGTCGTATTAATTTCGATAAGCCAGTAAGCAGTGGTTCTCTAGTTAGCCAGAGAGCTCTGCT
 ATATCACTCAGCATATAAGCTATTGGTCACTCGTACCCAAAGAGATCAATGGTCTCTCGAGACGA

 2600 2610 2620 2630 2640 2650 2660
 * * * * * * *
 TATATAGACCTCCCACCGTACACGCCAACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATT
 ATATATCTGGAGGGTGGCATGTGCGGATGGCGGGTAAACGCACTTACCCCGCTCAACAATGCTGTAAAA

 2670 2680 2690 2700 2710 2720 2730
 * * * * * * *
 GGAAAGTCCCCTGATTTGGTGCACAAACAAACTCCATTGACGTCATGGGGTGGAGACTGGAAATC
 CCTTCAGGGCAACTAAAACACGGTTTGTGAGGGTAACATGCACTTACCCACCTCTGAACCTTAC

 2740 2750 2760 2770 2780 2790 2800
 * * * * * * *
 CCCGTGAGTCACCCGCTATCCACGCCATTGATGTTACTGCCAACCGCATCACCATGGTAATAGCGAT
 GGGCACTCAGTTGGCGATAGGTGCGGGTAACATGACGGTTTGGCGTAGTGGTACCATATCGCTA

FIGURE 19 CONTINUED

2810 2820 2830 2840 2850 2860 2870
 * * * * * * *
 GACTAATACGTAGATGTAATGCCAAAGTAGGAAAGTCCCATAAGGTATGTAATGGGCATAATGCCAGGCG
 CTGATTATGCATCTACATGACGGTTATCCTTCAGGTATTCCAGTACATGACCCGTATTACGGTCCGC
 2880 2890 2900 2910 2920 2930 2940
 * * * * * * *
 GGCCATTACCGTCATTGACGTCATAGGGGGCCTACTGGCATATGATACACTTGATGTAATGCCAAGT
 CCCGTAAATGGCAGTAATGCACTGAGTTATCCCCCGCATGAACCGTATACTATGTGAACATGACGGTTCA
 2950 2960 2970 2980 2990 3000 3010
 * * * * * * *
 GGGCAGTTACCGTAAATAGTCACCCATTGACGTCATGGAAAGTCCCTATTGGCGTTACTATGGGAAC
 CCCGTCAAATGGCATTATCAGGTGGGTAAC TGAGTTACCTTCAGGATAACCGCAATGATAACCCCTG
 3020 3030 3040 3050 3060 3070 3080
 * * * * * * *
 ATACGTCAATTAGACGTCATGGGGGGCGTTGGCGGTCAAGCCAGGCGGGCATTACCGTAAGT
 TATGCAGTAATAACTGCACTTACCCGCCCAAGCAACCCCAAGTCGGTCCGCCGGTAAATGGCATTCA
 3090 3100 3110 3120 3130 3140 3150
 * * * * * * *
 TATGTAACGCGGAACCTCCATATGGGCTATGAACTAATGACCCCGTAATTGATTACTATTAATAACTAG
 ATACATTGCGCCTTGAGGTATAACCGATACTTGATTACTGGGCATTAACATGATAATTATTGATC
 3160 3170 3180 3190 3200 3210 3220
 * * * * * * *
 TCAATAATCAATGCTCTGCATTATGAATCGGCAACGCGCGGGAGAGGCGGTTTGCCTATTGGCGCT
 AGTTATTAGTTACAGGACGTAATTACTTACCGCTTGCCTCGCCCTCTCCGCCAAACGCATAACCGCGA
 3230 3240 3250 3260 3270 3280 3290
 * * * * * * *
 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCTGGCTGCGCGAGCGGTATCAGCTCACTC
 GAAGGCGAAGGAGCGAGTGACTGAGCGACCGAGCCAGCAAGCCGACCCGCTGCCATAGTCGAGTGAG
 3300 3310 3320 3330 3340 3350 3360
 * * * * * * *
 AAAGGCCTTAATACGGTTATCACAGAATCAGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAG
 TTCCGCCATTATGCCAATAGGTGTCTTAGTCCCTATTGCTCCTTGTACACTCGTTTCCGGTC
 3370 3380 3390 3400 3410 3420 3430
 * * * * * * *
 CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCTTTCCATAGGCTCCGCCCCCTGACGAGC
 GTTTCCGGTCCTTGGCATTTCCGGCACAAGACCGCAAAAGGTATCCGAGGGGGGGACTGCTCG
 3440 3450 3460 3470 3480 3490 3500
 * * * * * * *
 ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGGTTCC
 TAGTGTGTTAGCTGCGAGTTAGTCTCCACCGCTTGGCTGTCTGATATTCTATGGTCCGAAAGG

FIGURE 19 CONTINUED

3510 3520 3530 3540 3550 3560 3570
 * * * * * * *
 CCCTGGAAAGCTCCCTCGCGCTCTCCGTCCGACCCCTGCCGCTTACGGATACCTGTCCGCCCTTC
 GGGACCTCGAGGGAGCACCGAGAGGAAGCTGGACGGGAATGGCTATGGACAGGGAAAGAG

 3580 3590 3600 3610 3620 3630 3640
 * * * * * * *
 CCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTGGTAGGTCGTTGCT
 GGAAGCCCTTCGCACCGCGAAGAGTACAGTGCGACATCCATAGAGTCAGCCACATCCAGCAAGCGA

 3650 3660 3670 3680 3690 3700 3710
 * * * * * * *
 CCAAGCTGGGCTGTGACGAAACCCCCCGTTAGCCGACCGCTGCCCTATCCGTAACACTATCGTCT
 GGTCGACCCGACACACGTGCTGGGGGGCAAGTCGGCTGGGACGCGGAATAGGCCATTGATAGCAGA

 3720 3730 3740 3750 3760 3770 3780
 * * * * * * *
 TGAGTCCAACCCCGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG
 ACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGGTACCATGGCTTAATCGTCTCGC

 3790 3800 3810 3820 3830 3840 3850
 * * * * * * *
 AGGTATGTAGGGGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACACTACGGCTACACTAGAAGGACAGTAT
 TCCATACATCCGCCACGATGTCAGAACCTACCACGGATTGATGCCATGTGATCTTCCTGTCATA

 3860 3870 3880 3890 3900 3910 3920
 * * * * * * *
 TTGGTATCTGCCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACA
 AACCATAGACCGAGACGACTCGGTCAATGGAAGCCTTTCTCAACCATCGAGAACTAGGCCGTTGT

 3930 3940 3950 3960 3970 3980 3990
 * * * * * * *
 AACACCGCTGGTAGCGGTGTTTTGTTGCAAGCAGCAGATTACCGCGAGAAAAAAAAGGATCTAA
 TTGGTGGGACCATCGCCACCAACGTTCGTCTAATGCGCTTCTTTCTAGAGTT

 4000 4010 4020 4030 4040 4050 4060
 * * * * * * *
 GAAGATCTTGTATCTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTGG
 CTCTAGGAAACTAGAAAAGATGCCAGACTGCGACTCACCTGCTTTGAGTGCATTCCCTAAACCC

 4070 4080 4090 4100 4110 4120 4130
 * * * * * * *
 TCATGAAACAATAAAATGCTGTTACATAAACAGTAATACAAGGGGTGTTATGAGCCATATTCAACGGG
 AGTACTTGTATTTGACAGACGAATGTATGTCAATTGTCATTGCTTCCCACAAATCTGGTATAAGTTGCC

 4140 4150 4160 4170 4180 4190 4200
 * * * * * * *
 AAACGTCTTGTGCTGAGGCCCGGATTAAATCCAAACATGGATGCTGATTATATGGGTATAAAATGGGCTCG
 TTGCGAGAACGAGCTCCGGCGCTAATTAGGTTGACCTACGACTAAATACCCATATTACCCGAGC

FIGURE 19 CONTINUED

CGATAATGTCGGCAATCAGGTGCGACAATCTATGATTGGAGGCCGATGCAGAGTTGTT
GCTATTACAGCCGTTAGTCCACGCTGTTAGATAGCTAACATACCTTCGGCTACGCGTCTCARCAA
4210 4220 4230 4240 4250 4260 4270

CTGAAACATGGCAAAGGTAGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTGACGG
GACTTTGTAACCGTTCCATCGAACGGTTACTACAAATGTCTACTCTACAGTCTGATTGACCGACTGCC
4280 4290 4300 4310 4320 4330 4340

AATTTATGCCTTCCGACCATCAGCATTCTCGTACTCTGATGATGCATGGTTACTCACCACCTGC
TTAAATACGGAGAAGGCTGGTAGTCGTAAAATAGGCATGAGGACTACTACGTACCAATGAGTGGTGACG
4350 4360 4370 4380 4390 4400 4410

GATCCCCGGAAAACAGCATTCCAGGTATTAGAAGAATATCTGATTAGGTGAAAATATTGTTGATGCG
CTAGGGGCCCTTGTGTAAGGTCCATAATCTTATAGGACTAAGTCCACTTTATAACAACATACGC
4420 4430 4440 4450 4460 4470 4480

CTGGCAGTGTCTCGCCGGTTGATTGATTCGATTCTGTTGTAATTGTCCTTTAACAGCGATCGCGTAT
GACCGTCAGAGCACGGCCAACGTAAGCTAAGGACAAACATTAACAGGAAAATTGTCGCTAGCGCATA
4490 4500 4510 4520 4530 4540 4550

TTCGTCTCGCTAGGGCAATCAGGAATGAAACCGTTGGTATGCGAGTGATTTGACGAGCG
AAGCAGAGCGAGTCCGCTTAGTGCTTACTTATTGCCAACCAACTACGCTCACTAAACTACTGCTCGC
4560 4570 4580 4590 4600 4610 4620

TAATGGCTGGCTGTTGAACAAGTCTGGAAAGAAAATGCATAAACCTTGCATTCTCACCGGATTGAGTC
ATTACCGACGGACAACCTGTCAGACCTTCTACGTTATTGAAAACGTAAGAGTGGCCTAACGTCAG
4630 4640 4650 4660 4670 4680 4690

GTCACTCATGGTGATTCTCACTTGATAACCTTATTTTGACGAGGGGAAATTAAATGGTTGATGATG
CACTGAGTACCAACTAAAGAGTGAACATTGAAATAAAACTGCTCCCTTAATTATCCAACATAACTAC
4700 4710 4720 4730 4740 4750 4760

TTGGACGAGTCGGAATCGCAGACCGATAACCGAGTCTGCCATTGCTATGGAACTGCCTCGGTGAGTTTC
AACCTGCTCAGCCTTAGCGCTGGCTATGGCTAGAACGGTAGGATACCTTGACGGAGCCACTCAAAG
4770 4780 4790 4800 4810 4820 4830

TCCTTCATTACAGAAACGGCTTTCAAAAATGGTATTGATAACCTGATGATGAAATAATTGAGTTT
AGGAAGTAAATGCTTGTGCGAAAAGTTTATACCCATAACTATTAGGACTATACTTATTAAACGTCAAA
4840 4850 4860 4870 4880 4890 4900

FIGURE 19 CONTINUED

4910 4920 4930 4940 4950 4960 4970
* * * * * * *
CATTGATGCTCGATGAGTTCTAATCAGAATTGGTTAATTGGTGTAAACACTGGCAGAGCATCATGA
GTAAACTACGAGCTACTCAAAAAGATTAGTCTAACCAACATTGTGACCGTCTCGTAGTACT
4980 4990 5000 5010 5020 5030 5040
* * * * * * *
GCGGATACATATTTGAATGTATTAGAAAAATAACAAATAGGGGTTCCGCCACATTCCCCGAAAAGT
CGCCTATGTATAAACTTACATAAAATCTTTTATTTGTTATCCCCAAGGCCGTGTAAAGGGGCTTTCA
5050
*
GCCACCTGACGTC
CGGTGGACTGCAG

FIGURE 19 CONTINUED

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTCCTGTGGGTGCCCG						
CGATCGGGCGGTGGTACCCCTACGTCCACGTCTAGGTCTCGGACAAAGACGAGGAGGACACCCACGGGC						
M G M Q V Q I Q S L F L L L W V P>						
80	90	100	110	120	130	140
*	*	*	*	*	*	*
GGTCAGAGGACACACCCCTGTGGAAGGCGGAATCCTGTATAAGGCAAGTTCGTGGCTGCCTGGACCCCT						
CCAGGTCTCCTGTGTCGGACACCCCTCCGGCCTTAGGACATATTCCGGTCAAGCACCGACGGACCTGGGA						
G S R G H T L W K A G I L Y K A K F V A A W T L>						
150	160	170	180	190	200	210
*	*	*	*	*	*	*
GAAGGCTGCCGTTTCTGCTTAGCGATTCTTCCTAGCGTAAGCTGACCCACTGTGCGTGACCCCTG						
CTTCCGACGGCGAAAGGACGGATCGCTAACGAAAGGATCGCACTTCGACTGGGTGACACGCACTGGGAC						
K A A A F L P S D F F P S V K L T P L C V T L>						
220	230	240	250	260	270	280
*	*	*	*	*	*	*
TATATGGATGACGTGGTGTGGAGCCAGCATCATCAACTTCGAGAAGCTGGACTGTCCAGATACTGG						
ATATACCTACTGCACCACGACCCCTCGGTCTAGTAGTTGAAGCTTTCGACCCCTGACAGGTCTATGCACC						
Y M D D V V L G A S I I N F E K L G L S R Y V>						
290	300	310	320	330	340	350
*	*	*	*	*	*	*
CTAGGCTGATCCTGAAGGAGCTGTGCACGGCGTGTCCACCCCTGCCAGAGACCAACCGTGGTGGAGGAC						
GATCCGACTAGGACTTCCTCGACACGTGCCGCACAGTGGGACGGTCTCTGGTGGCACCACTCCTCCTG						
A R L I L K E P V H G V S T L P E T T V V R R T>						
360	370	380	390	400	410	
*	*	*	*	*	*	
CGTGACTATGGAGTGCCTGTGGAAAGTGGCTGAGCTGCTGGTGCCTTGTGGGTACC						
GCACATGATACTCACGGACACCTTCACCGACTCGGACGACCACGGAAACACCCATGG						
V Y Y G V P V W K W L S L L V P F V G T>						

FIGURE 20

10	20	30	40	50	60	70	
*	*	*	*	*	*	*	*
GCTAGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCCTGTGGGTGCCG							
CGATCGCGCGGTGGTACCCCTACGTCCACGTCTAGGTCTGGACAAAGACGAGGAGGACACCCACGGC							
M	G	M	Q	V	Q	I	P>
80	90	100	110	120	130	140	
*	*	*	*	*	*	*	*
GGTCAGAGGACACACCCCTGTGGAAGGCCGAATCCTGTATAAGGCAAGTCGTGGCTGCCCTGGACCCCT							
CCAGGTCTCCTGTGTGGGACACCTTCCGGCTTAGGACATATTCCGGTTCAAGCACCGACGGACCTGGGA							
G	S	R	G	H	T	L	W>
150	160	170	180	190	200	210	
*	*	*	*	*	*	*	*
GAAGGCTGCCGCTTCTGCCAGATTCTTCTAGCGTAAGCTGACCCCCACTGTGGCTGACCCCTG							
CTTCCGACGGCGAAAGGACGGATCGCTAAAGAAGGATCGCACTTCGACTGGGGTGACACGCACGGAC							
K	A	A	A	F	L	P	S>
220	230	240	250	260	270	280	
*	*	*	*	*	*	*	*
TATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGATCCTGAAGGAGCCTG							
ATATACTACTGCACCACGACCCCTCACCTGACAGGTCCATGCACCGATCCGACTAGGACTCCTCGGAC							
Y	M	D	D	V	V	L	G>
290	300	310	320	330	340	350	
*	*	*	*	*	*	*	*
TGCAAGGGCTGTCCACCCCTGCCAGAGACCAACCGTGGTGAGGAGGACCGTGTACTATGGAGTGCCGTGTG							
ACGTGGCGACAGGTGGGACGGTCTCTGGTGGCACCACTCCTCTGGCACATGATAACCTCACGGACACAC							
V	H	G	V	S	T	L	P>
360	370	380	390				
*	*	*	*				
GAAGTGGCTGAGCCTGCTGGTGCCTTGTGTGAGGTAC							
CTTCACCGACTCGGACGACCACGGAAACACACTCCATGG							
K	W	L	S	L	L	V	P>
F V * >							

FIGURE 21

Figure 22

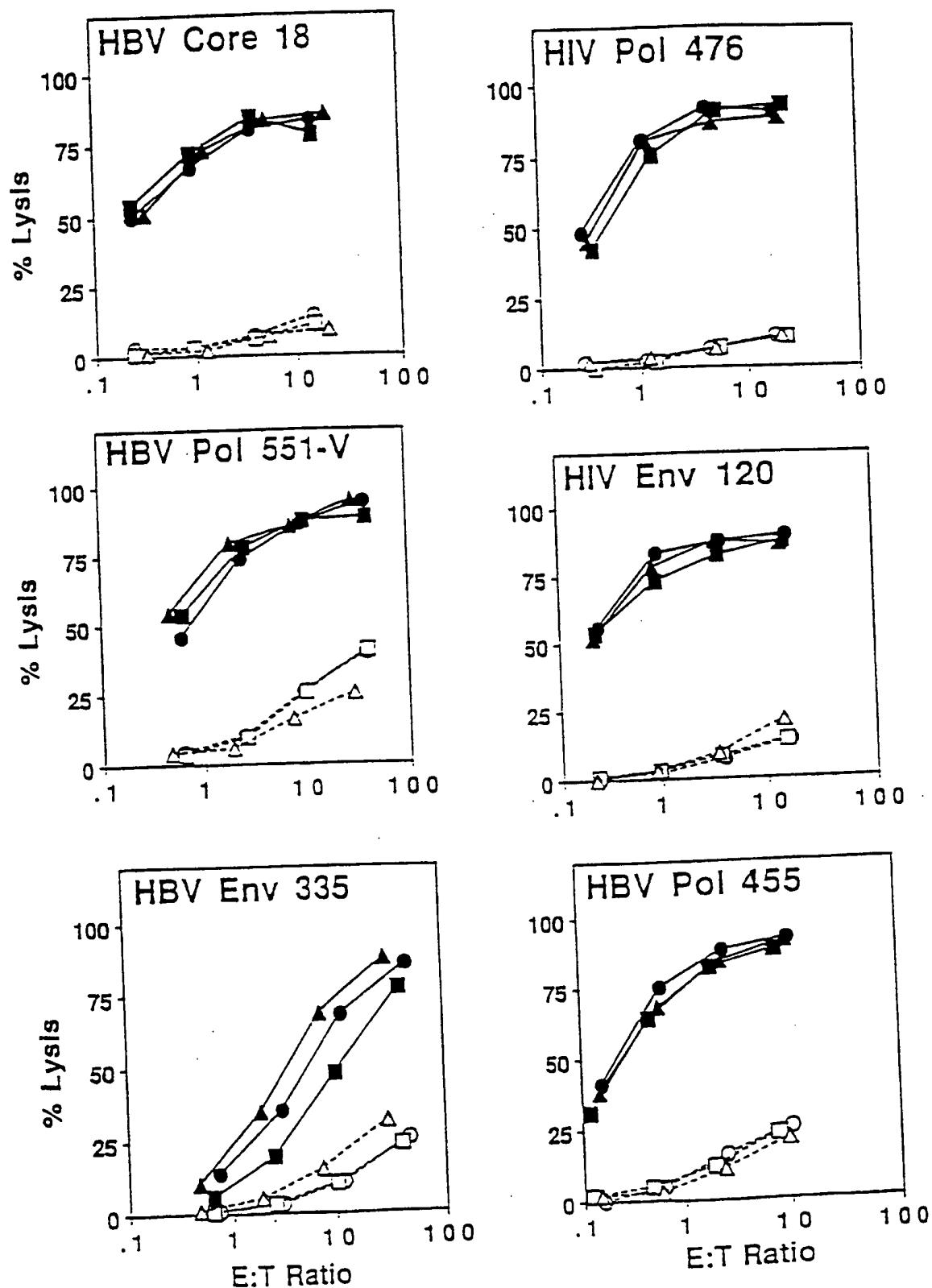


Figure 23

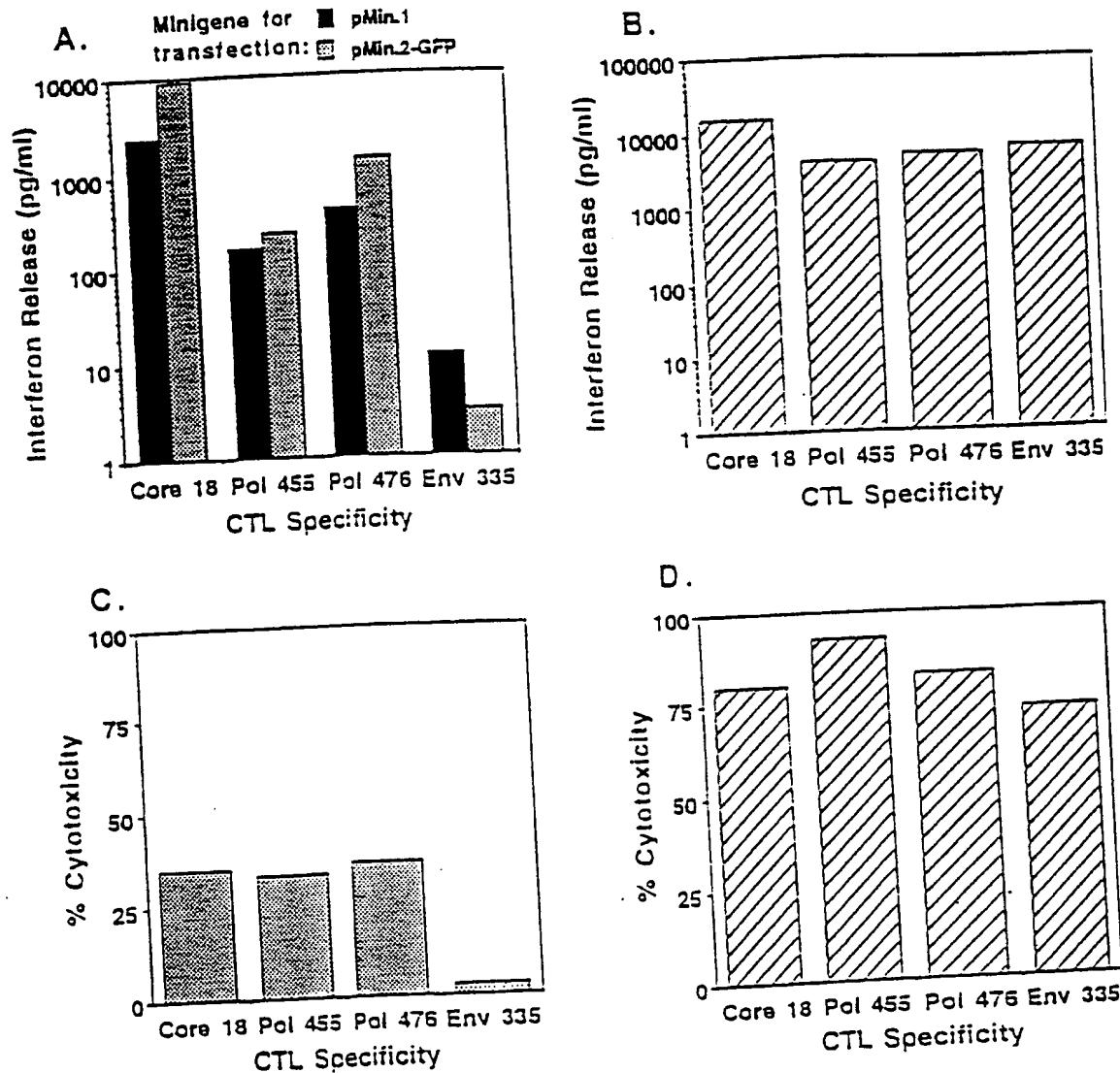


Figure 24

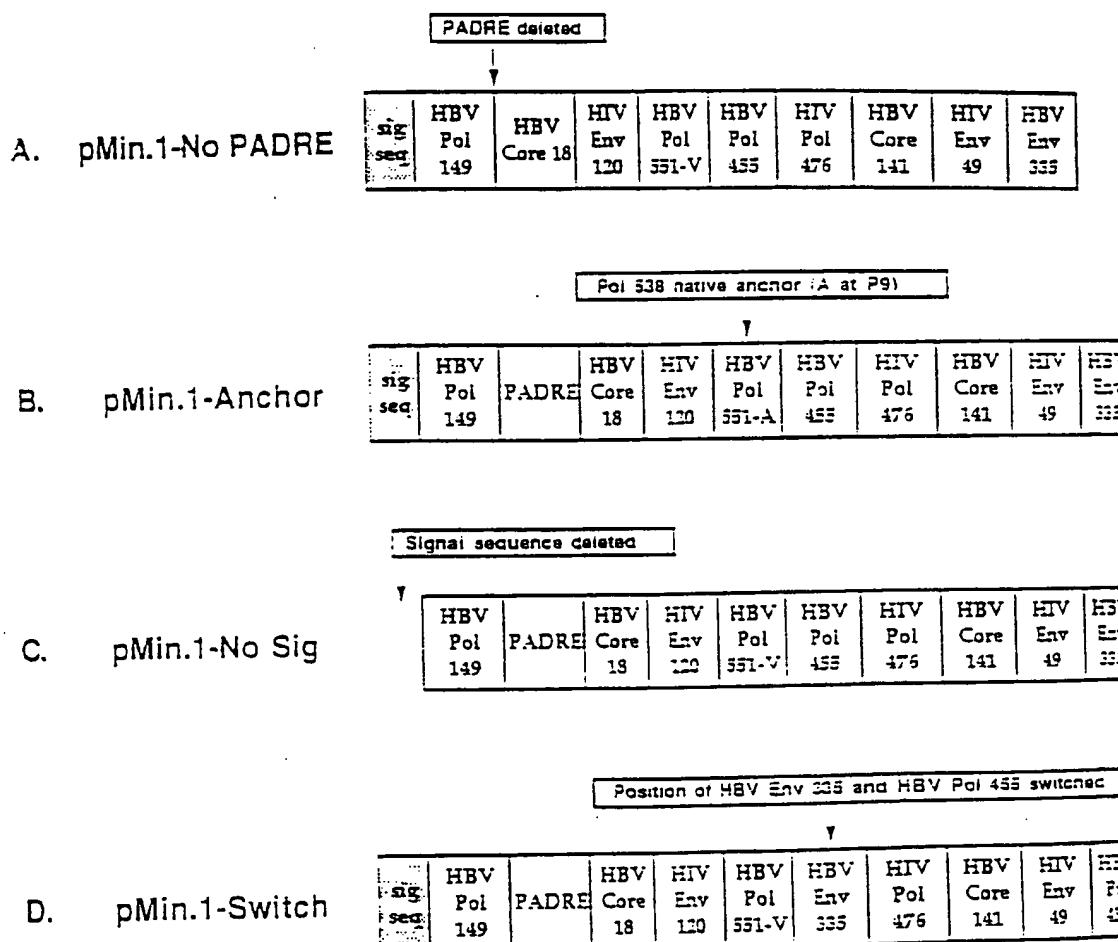


Figure 25

